SEQUENCE LISTING

<110> MACK, DAVID
      GISH, KURT

<120> NOVEL METHODS OF DIAGNOSING AND TREATING BREAST CANCER,
      COMPOSITIONS, AND METHODS OF SCREENING FOR BREAST
      CANCER MODULATORS

<130> A-67860-3/DJB/JJD

<140> US 09/525,361
<141> 2000-03-15

<150> US 09/268,865
<151> 1999-03-15

<150> US 09/450,810
<151> 1999-11-29

<150> US 09/453,137
<151> 1999-12-02

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<151> 1999-11-12

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<151> 2000-03-08

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<170> PatentIn Ver. 2.1

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3

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Asp Tyr Thr Ala Thr Ile Tyr Leu Arg Gln Arg Trp Met Asp Gln Arg
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Leu Val Phe Glu Gly Asn Lys Ser Phe Thr Leu Asp Ala Arg Leu Val
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Glu Phe Leu Trp Val Pro Asp Thr Tyr Ile Val Glu Ser Lys Lys Ser
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Gln Leu Glu Ser Trp Gly Tyr Asp Gly Asn Asp Val Glu Phe Thr Trp
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Ala Arg Thr Cys Ile Gly Val Thr Thr Val Leu Ser Met Thr Thr Leu
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4

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Arg Ile Val Asp Tyr Phe Thr Ile Gln Asn Pro Ser Asn Val Asp His
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Tyr Ser Lys Leu Leu Phe Pro Leu Ile Phe Met Leu Ala Asn Val Phe
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        35              40                  45

Ser Val Thr Glu Ser Pro Gln Arg Val Ile Ile Thr Glu Asp Asp Glu
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Asp Glu Thr Thr Val Glu Leu Glu Gly Gln Asp Glu Asn Gln Glu Gly
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Asp Phe Glu Asp Ala Asp Thr Gln Glu Gly Asp Thr Glu Ser Glu Pro
                85              90                  95

Tyr Asp Asp Glu Glu Phe Glu Gly Tyr Glu Asp Lys Pro Asp Thr Ser
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Leu Gln Asn Ser Trp Glu Ser Tyr Tyr Leu Glu Ile Leu Met Val Thr
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Ser Thr Gly Lys Leu Asn Gln Glu Asn Glu His Ile Tyr Asn Leu Trp
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Cys Ser Gly Arg Val Cys Cys Glu Gly Met Leu Ile Gln Leu Arg Phe
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Leu Lys Arg Gln Asp Leu Leu Asn Val Leu Ala Arg Met Met Arg Pro
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Asp Thr Tyr Val Phe Ala Val Gly Thr Arg Lys Ala Leu Val Arg Leu
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Asp Pro Glu Lys Gln Arg Arg Leu Glu Glu Ala Ala Leu Arg Arg Asp
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<210> 10
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 10
Lys Phe Asp Asp Phe Glu Asp Glu Glu Asp Ile Val Glu Tyr Cys
  1   5   10   15

<210> 11
<211> 1958
<212> DNA
<213> Homo sapiens

<400> 11
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gcgagcgctg ccgctggatc ctgcccctgc tcctactcag cgccatcgcc ttcgacatca 180
tcgcgctggc cggccgcggc tggttgcagt ctagcgacca cggccagacg tcctcgctgt 240
ggtggaaatg ctcccaagag ggcggcggca gcgggtccta cgaggagggc tgtcagagcc 300
tcatggagta cgcgtggggt agagcagcgg ctgccatgct cttctgtggc ttcatcatcc 360
tggtgatctg tttcatcctc tccttcttcg ccctctgtgg accccagatg cttgtcttcc 420
tgagagtgat tggaggtctc cttgccttgg ctgctgtgtt ccagatcatc tccctggtaa 480
tttaccccgt gaagtacacc cagaccttca cccttcatgc caaccctgct gtcacttaca 540
tctataactg ggcctacggc tttgggtggg cagccacgat tatcctgatt ggctgtgcct 600
tcttcttctg ctgcctcccc aactacgaag atgaccttct gggcaatgcc aagcccaggt 660
acttctacac atctgcctaa cttgggaatg aatgtgggag aaaatcgctg ctgctgagat 720
ggactccaga agaagaaact gtttctccag gcgactttga acccattttt tggcagtgtt 780
catattatta aactagtcaa aaatgctaaa ataatttggg agaaaatatt ttttaagtag 840
tgttatagtt tcatgtttat cttttattat gttttgtgaa gttgtgtctt ttcactaatt 900
acctatacta tgccaatatt tccttatatc tatccataac atttatacta catttgtaag 960
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agaagaggaa gataaggtta aagttgtta atgaccaaac attctaaaag aaatgcaaaa 1140
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atgttcagaa ccagagtaga ctggattgaa agatggactg ggtctaattt atcatgactg 1500
atagatctgg ttaagttgtg tagtaaagca ttaggagggt cattcttgtc acaaaagtgc 1560
cactaaaaca gcctcaggag aataaatgac ttgctttttct aaatctcagg tttatctggg 1620

10

```
ctctatcata tagacaggct tctgatagtt tgcaactgta agcagaaacc tacatatagt 1680
taaaatcctg gtctttcttg gtaaacagat tttaaatgtc tgatataaaa catgccacag 1740
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tatgattttt taccatttcg acttacataa tgaaaaccaa ttcattttaa atatcagatt 1860
attattttgt aagttgtgga aaaagctaat tgtagttttc attatgaagt tttcccaata 1920
aaccaggtat tctaaacttg aaaaaaaaaa aaaaaaaa                           1958
```

<210> 12
<211> 582
<212> DNA
<213> Homo sapiens

<400> 12
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agcgccatcg ccttcgacat catcgcgctg gccggccgcg gctggttgca gtctagcgac 120
cacggccaga cgtcctcgct gtggtggaaa tgctcccaag agggcggcgg cagcgggtcc 180
tacgaggagg gctgtcagag cctcatggag tacgcgtggg gtagagcagc ggctgccatg 240
ctcttctgtg gcttcatcat cctggtgatc tgtttcatcc tctccttctt cgccctctgt 300
ggaccccaga tgcttgtctt cctgagagtg attggaggtc tccttgcctt ggctgctgtg 360
ttccagatca tctcccctggt aatttacccc gtgaagtaca cccagacctt caccctttcat 420
gccaaccctg ctgtcactta catctataac tgggcctacg gctttgggtg ggcagccacg 480
attatcctga ttggctgtgc cttcttcttc tgctgcctcc ccaactacga agatgacctt 540
ctgggcaatg ccaagcccag gtacttctac acatctgcct aa                     582
```

<210> 13
<211> 193
<212> PRT
<213> Homo sapiens

<400> 13
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Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
 1               5                   10                  15

Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly
            20                  25                  30

Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp
        35                  40                  45

Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly
    50                  55                  60

Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Met
65                  70                  75                  80

Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys Phe Ile Leu Ser Phe
                85                  90                  95

Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly
```

11

Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile Leu Ser Leu Val Ile
     115   120   125

Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu His Ala Asn Pro Ala
     130   135   140

Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
145   150   155   160

Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys Cys Leu Pro Asn Tyr
          165   170   175

Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser
          180   185   190

Ala

<210> 14
<211> 193
<212> PRT
<213> Mouse

<400> 14
Met Leu Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
  1   5   10   15

Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly
        20   25   30

Arg Gly Trp Leu Gln Ser Ser Asn His Ile Gln Thr Ser Ser Leu Trp
      35   40   45

Trp Arg Cys Phe Asp Glu Gly Gly Gly Ser Gly Ser Tyr Asp Asp Gly
  50   55   60

Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg Ala Ala Ala Ala Thr
65   70   75   80

Leu Phe Cys Gly Phe Ile Ile Leu Cys Ile Cys Phe Ile Leu Ser Phe
        85   90   95

Phe Ala Leu Cys Gly Pro Met Gln Leu Val Phe Leu Arg Val Ile Gly
        100   105   110

Gly Leu Leu Ala Leu Ala Ala Ile Phe Gln Ile Leu Ser Leu Val Ile
     115   120   125

```
Tyr Pro Val Lys Tyr Thr Gln Thr Phe Arg Leu His Asp Asn Pro Ala
    130                 135             140

Val Asn Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr
145         .       150             155             160

Ile Ile Leu Ile Gly Cys Ser Phe Phe Phe Cys Cys Leu Pro Asn Tyr
                165             170             175

Glu Asp Asp Leu Leu Gly Ala Ala Lys Pro Arg Tyr Phe Tyr Pro Pro
            180             185             190

Ala
```

```
<210> 15
<211> 124
<212> PRT
<213> Rat

<400> 15
Glu Tyr Ala Trp Gly Arg Ala Ala Ala Thr Leu Phe Cys Gly Phe
 1           5               10                  15

Ile Ile Leu Val Ile Cys Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly
            20          25                  30

Pro Gln Met Leu Val Phe Leu Arg Val Ile Gly Gly Leu Leu Ala Leu
        35              40                  45

Ala Ala Val Phe Gln Ile Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr
    50              55                  60

Thr Gln Thr Phe Arg Leu His Asp Asn Pro Ala Val Asn Tyr Ile Tyr
65              70              75                  80

Asn Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly
                85              90                  95

Cys Ser Phe Phe Phe Cys Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu
                100             105             110

Gly Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser Ala
            115             120
```

```
<210> 16
<211> 15
<212> PRT
<213> Artificial Sequence
```

13

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 16
Cys Ser Tyr Ser Ala Pro Ser Pro Ser Thr Ser Ser Arg Trp Pro
1   5   10   15

<210> 17
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 17
Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro
1   5   10   15

<210> 18
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 18
Cys Gly Gly Asn Ala Pro Lys Arg Gly Gly Gly Arg Gly Ser Tyr
1   5   10   15

<210> 19
<211> 1970
<212> DNA
<213> Mouse

<400> 19
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tcttcggggg agccgcctct tccttwattc ggckcygaca gcgctcgcag gaccactctt 120
ggccgctgct cctgcccggc gttcctccgc tccgcgcccg ccgccaccga cgacatgctg 180
cgctgcggcc tggcctgcga gcgctgcagg tggatcctgc ccctgctgct gctcagcgcc 240
atcgccttcg acatcatcgc gctggccggc cgcggctggc tgcagtctag caaccacatc 300
cagacatcgt cgctttggtg gaggtgtttc gacgagggcg gcggcagcgg ctcctacgac 360
gatggctgcc agagcctcat ggagtacgca tggggacgag cagctgcagc cacgcttttc 420
tgtggcttta tcatcctgtg catctgcttc attctctcgt tcttcgccct gtgtggaccc 480
cagatgcttg ttttcctgag agtcattgga ggcctcctcg cactggctgc catattccag 540
atcatctccc tggtaatcta ccccgtgaag tacacacaga ccttcaggct tcacgataac 600
cctgctgtta attacatcta taactgggcc tatggcttcg gatgggcggc caccatcatc 660

```
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gccgccaagc ccaggtactt ctatccccca gcctaatgtg ggaggaagag cctgagaaaa 780
gcctgctgca agatggatct gaggaggaaa ctgttctcca aggcacaagg aacctacgtt 840
tgggcaatgt tcatatgatc agaaatgtta gaataaatgc taaagaaaat tcttcataat 900
tagtgttaag tttcatgtat gtcgtgtgga gttaaaaaga cttgaattct gtttgctaag 960
tatatgctaa ttttttcctta tgtcaattct ataccattta agcttcattt gttaaagaat 1020
atgcctgtga aacttgataa ggtagaaatg gagcagcctc tcatttaata atctgatggg 1080
gcttctgttt ttccacatag aatgggttgt ttctgctaag ggctacagag gaggaaagtc 1140
actggcaaaa cttccatgac caaatatcct gaaattagtt tgtttttttt taaaagacct 1200
tattttgagt tttcagttac ataaagaagc agaagcagat tggtttccta agtgagcatc 1260
atttgtgaga attttttagtc agtgttttga acaattattg ttttctaag cttcatgttg 1320
actttctctg atgcgtagaa aagtgttcta acgtggctga ggttaagccg ctgtcattac 1380
tgaaatgcta agaattttcc tcttttcccg tagtgtagag gggtagggtg tgggcagaag 1440
ccgtgttagc acatctgtag tattgtgtgt gtatgcttag aaccagcgta gaccggatgg 1500
gaggatggac taggcctaat ccctcccaac tggtggatgt gaagaggtca ggtaggaagg 1560
cacaggaggg tcaccactgt cacagcagtg ccatgcagac atcctaggag aagacatggc 1620
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ataccggaag ggctactatt acctttttct taccatttat acttacctaa tggaaacgag 1860
cttgttttaa ctatcagaac actattttgt aaggtgctgc aaagacagtt gaagtttтca 1920
ttaccaattt ccccaataaa ccaggtgttc aaatcctgaa aaaaaaaggc        1970
```

<210> 20
<211> 582
<212> DNA
<213> Mouse

<400> 20
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cacatccaga catcgtcgct ttggtggagg tgtttcgacg agggcggcgg cagcggctcc 180
tacgacgatg gctgccagag cctcatggag tacgcatggg gacgagcagc tgcagccacg 240
cttttctgtg gctttatcat cctgtgcatc tgcttcattc tctcgttctt cgccctgtgt 300
ggaccccaga tgcttgtttt cctgagagtc attggaggcc tcctcgcact ggctgccata 360
ttccagatca tctccctggt aatctacccc gtgaagtaca cacagacctt caggcttcac 420
gataaccctg ctgttaatta catctataac tgggcctatg gcttcggatg ggcggccacc 480
atcatcttga ttggttgttc cttcttcttc tgctgcctcc ccaactacga ggatgacctt 540
ttggggggccg ccaagcccag gtacttctat cccccagcct aa           582
```

<210> 21
<211> 536
<212> DNA
<213> Rat

<400> 21
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gaatacgcct ggggccgagc agctgctgcc actctcttct gtggattcat catcctggtc 60
atctgcttca tcctctcgtt cttcgccctg tgtggacccc agatgcttgt tttcctgaga 120
gtgattggag gccttctcgc actggctgct gtattccaga tcatctccct ggttatctat 180
```

```
cccgtgaagt acacacaaac cttcaggctt catgataatc ccgctgttaa ttacatctac 240
aactgggcct atggcttcgg atgggcagcc acgatcatct tgattggttg ctcttttcttc 300
ttctgctgcc tccccaacta cgaggatgac cttctgggca atgcaaagcc caggtacttc 360
tatacatctg cctaatgtgg agggagatcc tgagaaaagc ctgctgcaag atgcatgtga 420
ggaggaaagt gttctccaag gagcaaagaa cctatgtttg ggcagtgttc atatgagtgg 480
aaatgctaga ataaatgcta aagaaaattc ttcataaaaa aaaaaaaaaa aaaaaa     536
```

```
<210> 22
<211> 375
<212> DNA
<213> Rat
```

```
<400> 22
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gtgattggag gccttctcgc actggctgct gtattccaga tcatctccct ggttatctat 180
cccgtgaagt acacacaaac cttcaggctt catgataatc ccgctgttaa ttacatctac 240
aactgggcct atggcttcgg atgggcagcc acgatcatct tgattggttg ctcttttcttc 300
ttctgctgcc tccccaacta cgaggatgac cttctgggca atgcaaagcc caggtacttc 360
tatacatctg cctaa                                                 375
```

```
<210> 23
<211> 471
<212> DNA
<213> Homo sapiens
```

```
<400> 23
ctttgaagca tttttgtctg tgctccctga tcttcaggtc accaccatga agttcttagc 60
agtcctggta ctcttgggag tttccatctt tctggtctct gcccagaatc cgacaacagc 120
tgctccagct gacacgtatc cagctactgg tcctgctgat gatgaagccc ctgatgctga 180
aaccactgct gctgcaacaa ctgcgaccac tgctgctcct accactgcaa ccaccgctgc 240
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tggtagagtg tgtccctgag atggaatcag cttgagtctt ctgcaattgg gtcacaacta 360
ttcatgcttc ctgtgatttc atccaactac ttaccttgcc tacgatatcc cctttatctc 420
taatcagttt attttctttc aaataaaaaa taactatgag cgagctaaca t          471
```

```
<210> 24
<211> 273
<212> DNA
<213> Homo sapiens
```

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<400> 24
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aatccgacaa cagctgctcc agctgacacg tatccagcta ctggtcctgc tgatgatgaa 120
gcccctgatg ctgaaaccac tgctgctgca accactgcga ccactgctgc tcctaccact 180
gcaaccaccg ctgcttctac cactgctcgt aaagacattc cagttttacc caaatgggtt 240
ggggatctcc cgaatggtag agtgtgtccc tga                             273
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16

<210> 25
<211> 90
<212> PRT
<213> Homo sapiens

<400> 25
Met Lys Phe Leu Ala Val Leu Val Leu Leu Gly Val Ser Ile Phe Leu
 1   5   10   15

Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro
            20   25   30

Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu Thr Thr Ala
            35   40   45

Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr Ala Thr Thr Ala
        50   55   60

Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val Leu Pro Lys Trp Val
65   70   75   80

Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
                85   90

<210> 26
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 26
Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr Tyr Pro Ala Cys
 1   5   10   15

<210> 27
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 27
Leu Pro Lys Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
 1   5   10   15

17

<210> 28
<211> 1555
<212> DNA
<213> Homo sapiens

<400> 28
ggagttttct ggagctgttg caatgtgtat gctggtgaaa tctacttgag cattaagcag 60
tatctcccag cattgttagc tactgagtgg cacatcttca gtacgcatga ttcgtggggg 120
actcaggcag aggtaaaagt gtgaaacttt tcagcattac ctaagaagca aaggctcaat 180
tttggctgct tcattcttat ctcttctgcc acagttctaa cgtgcctgat ctactgagac 240
caaggatgac caatgactca gaagggaaaa tgggatttaa acacccaaag atcatgggga 300
atttcagagg tcatgccctc cctggaacct tcttttttat tattggtctt tggtggtgta 360
caaagagtat tctgaagtat atctgcaaaa agcaaaagcg aacctgctat cttggttcca 420
aaacattatt ctatcgattg gaaattttgg agggaattac aatagttggc atggctttaa 480
ctggcatggc tggggagcag tttattcctg gagggcccca tctgatgtta tatgactata 540
aacaaggtca ctggaatcaa ctcctgggct ggcatcattt caccatgtat ttcttctttg 600
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ccaagttaat gttgtcaaat gcctatttg tggaggcctt tatcttctac aaccacactc 720
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aaagttggat gcccacacta tgaaagaaat atttgtttta tttgccttat agatatgctc 1440
aaggttactg ggcttgctac tatttgtaac tccttgacca tggaattata cttgtttatc 1500
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<210> 29
<211> 291
<212> PRT
<213> Homo sapiens

<400> 29
Met Thr Asn Asp Ser Glu Gly Lys Met Gly Phe Lys His Pro Lys Ile
1   5   10   15

Met Gly Asn Phe Arg Gly His Ala Leu Pro Gly Thr Phe Phe Phe Ile
                20   25   30

Ile Gly Leu Trp Trp Cys Thr Lys Ser Ile Leu Lys Tyr Ile Cys Lys
            35   40   45

Lys Gln Lys Arg Thr Cys Tyr Leu Gly Ser Lys Thr Leu Phe Tyr Arg
        50   55   60

18

```
Leu Glu Ile Leu Glu Gly Ile Thr Ile Val Gly Met Ala Leu Thr Gly
 65                      70                  75                  80

Met Ala Gly Glu Gln Phe Ile Pro Gly Gly Pro His Leu Met Leu Tyr
                 85                  90                  95

Asp Tyr Lys Gln Gly His Trp Asn Gln Leu Leu Gly Trp His His Phe
            100                 105                 110

Thr Met Tyr Phe Phe Phe Gly Leu Leu Gly Val Ala Asp Ile Leu Cys
        115                 120                 125

Phe Thr Ile Ser Ser Leu Pro Val Ser Leu Thr Lys Leu Met Leu Ser
    130                 135                 140

Asn Ala Leu Phe Val Glu Ala Phe Ile Phe Tyr Asn His Thr His Gly
145                 150                 155                 160

Arg Glu Met Leu Asp Ile Phe Val His Gln Leu Leu Val Leu Val Val
            165                 170                 175

Phe Leu Thr Gly Leu Val Ala Phe Leu Glu Phe Leu Val Arg Asn Asn
        180                 185                 190

Val Leu Leu Glu Leu Leu Arg Ser Ser Leu Ile Leu Leu Gln Gly Ser
        195                 200                 205

Trp Phe Phe Gln Ile Gly Phe Val Leu Tyr Pro Pro Ser Gly Gly Pro
    210                 215                 220

Ala Trp Asp Leu Met Asp His Glu Asn Ile Leu Phe Leu Thr Ile Cys
225                 230                 235                 240

Phe Cys Trp His Tyr Ala Val Thr Ile Val Ile Val Gly Met Asn Tyr
            245                 250                 255

Ala Phe Ile Thr Trp Leu Val Lys Ser Arg Leu Lys Arg Leu Cys Ser
        260                 265                 270

Ser Glu Val Gly Leu Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu
        275                 280                 285

Glu Glu Met
    290


<210> 30
<211> 15
<212> PRT
<213> Artificial Sequence
```

19

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 30
Tyr Pro Pro Ser Gly Gly Pro Ala Trp Asp Leu Met Asp His Cys
1   5   10   15

<210> 31
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 31
Cys Leu Lys Asn Ala Glu Arg Glu Gln Glu Ser Glu Glu Glu Met
1   5   10   15

<210> 32
<211> 10320
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> (10123)..(10185)
<223> "n" at positions 10123 and 10185 can be any base.

<400> 32
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20

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21

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23

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Lys Asn Lys Glu Phe Ser Ala Asp Gln Met Ser Glu Asn Thr Asp Gln
            35                  40                  45

Ser Asp Ala Ala Glu Leu Asn His Lys Glu Glu His Ser Leu His Val
        50                  55                  60

Gln Asp Pro Ser Ser Ser Ser Lys Lys Asp Leu Lys Ser Ala Val Leu
65                  70                  75                  80

Ser Glu Lys Ala Gly Phe Asn Tyr Glu Ser Pro Ser Lys Gly Gly Asn
                85                  90                  95

Phe Pro Ser Phe Pro His Asp Glu Val Thr Asp Arg Asn Met Leu Ala
            100                 105                 110

Phe Ser Ser Pro Ala Ala Gly Gly Val Cys Glu Pro Leu Lys Ser Pro
            115                 120                 125

Gln Arg Ala Glu Ala Asp Asp Pro Gln Asp Met Ala Cys Thr Pro Ser
    130                 135                 140

Gly Asp Ser Leu Glu Thr Lys Glu Asp Gln Lys Met Ser Pro Lys Ala
145                 150                 155                 160

Thr Glu Glu Thr Gly Gln Ala Gln Ser Gly Gln Ala Asn Cys Gln Gly
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Leu Ser Pro Val Ser Val Ala Ser Lys Asn Pro Gln Val Pro Ser Asp
            180                 185                 190

Gly Gly Val Arg Leu Asn Lys Ser Lys Thr Asp Leu Leu Val Asn Asp
            195                 200                 205

Asn Pro Asp Pro Ala Pro Leu Ser Pro Glu Leu Gln Asp Phe Lys Cys
    210                 215                 220

Asn Ile Cys Gly Tyr Gly Tyr Tyr Gly Asn Asp Pro Thr Asp Leu Ile
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Asp Ala Glu Leu Asp Ser Lys Ile Leu Ala Leu His Asn Met Val Gln
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Phe Ser His Ser Lys Asp Phe Gln Lys Val Asn Arg Ser Val Phe Ser
            275             280             285

Gly Val Leu Gln Asp Ile Asn Ser Ser Arg Pro Val Leu Leu Asn Gly
    290             295             300

Thr Tyr Asp Val Gln Val Thr Ser Gly Gly Thr Phe Ile Gly Ile Gly
305             310             315             320

Arg Lys Thr Pro Asp Cys Gln Gly Asn Thr Lys Tyr Phe Arg Cys Lys
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Phe Cys Asn Phe Thr Tyr Met Gly Asn Ser Ser Thr Glu Leu Glu Gln
            340             345             350

His Phe Leu Gln Thr His Pro Asn Lys Ile Lys Ala Ser Leu Pro Ser
            355             360             365

Ser Glu Val Ala Lys Pro Ser Glu Lys Asn Ser Asn Lys Ser Ile Pro
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Ala Leu Gln Ser Ser Asp Ser Gly Asp Leu Gly Lys Trp Gln Asp Lys
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Ile Thr Val Lys Ala Gly Asp Asp Thr Pro Val Gly Tyr Ser Val Pro
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Ile Lys Pro Leu Asp Ser Ser Arg Gln Asn Gly Thr Glu Ala Thr Ser
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Tyr Tyr Trp Cys Lys Phe Cys Ser Phe Ser Cys Glu Ser Ser Ser Ser
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Leu Lys Leu Leu Glu His Tyr Gly Lys Gln His Gly Ala Val Gln Ser
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Gly Gly Leu Asn Pro Glu Leu Asn Asp Lys Leu Ser Arg Gly Ser Val
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Ile Asn Gln Asn Asp Leu Ala Lys Ser Ser Glu Gly Glu Thr Met Thr
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Lys Thr Asp Lys Ser Ser Ser Gly Ala Lys Lys Lys Asp Phe Ser Ser
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25

Lys Gly Ala Glu Asp Asn Met Val Thr Ser Tyr Asn Cys Gln Phe Cys
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Pro Leu Leu Arg His Tyr Gln Gln Leu His Asn Ile His Lys Cys Thr
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Ile Lys His Cys Pro Phe Cys Pro Arg Gly Leu Cys Ser Pro Glu Lys
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His Leu Gly Glu Ile Thr Tyr Pro Phe Ala Cys Arg Lys Ser Asn Cys
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Ser His Cys Ala Leu Leu Leu His Leu Ser Pro Gly Ala Ala Gly
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Ser Ser Arg Val Lys His Gln Cys His Gln Cys Ser Phe Thr Thr Pro
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Asp Val Asp Val Leu Leu Phe His Tyr Glu Ser Val His Glu Ser Gln
625   630   635   640

Ala Ser Asp Val Lys Gln Glu Ala Asn His Leu Gln Gly Ser Asp Gly
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Gln Gln Ser Val Lys Glu Ser Lys Glu His Ser Cys Thr Lys Cys Asp
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Phe Ile Thr Gln Val Glu Glu Glu Ile Ser Arg His Tyr Arg Arg Ala
        675   680   685

His Ser Cys Tyr Lys Cys Arg Gln Cys Ser Phe Thr Ala Ala Asp Thr
    690   695   700

Gln Ser Leu Leu Glu His Phe Asn Thr Val His Cys Gln Glu Gln Asp
705   710   715   720

Ile Thr Thr Ala Asn Gly Glu Glu Asp Gly His Ala Ile Ser Thr Ile
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Lys Glu Glu Pro Lys Ile Asp Phe Arg Val Tyr Asn Leu Leu Thr Pro
            740   745   750

Asp Ser Lys Met Gly Glu Pro Val Ser Glu Ser Val Val Lys Arg Glu
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Lys Leu Glu Glu Lys Asp Gly Leu Lys Glu Lys Val Trp Thr Glu Ser
770   775   780

26

Ser Ser Asp Asp Leu Arg Asn Val Thr Trp Arg Gly Ala Asp Ile Leu
785   790   795   800

Arg Gly Ser Pro Ser Tyr Thr Gln Ala Ser Leu Gly Leu Leu Thr Pro
          805   810   815

Val Ser Gly Thr Gln Glu Gln Thr Lys Thr Leu Arg Asp Ser Pro Asn
          820   825   830

Val Glu Ala Ala His Leu Ala Arg Pro Ile Tyr Gly Leu Ala Val Glu
          835   840   845

Thr Lys Gly Phe Leu Gln Gly Ala Pro Ala Gly Gly Glu Lys Ser Gly
    850   855   860

Ala Leu Pro Gln Gln Tyr Pro Ala Ser Gly Glu Asn Lys Ser Lys Asp
865   870   875   880

Glu Ser Gln Ser Leu Leu Arg Arg Arg Arg Gly Ser Gly Val Phe Cys
              885   890   895

Ala Asn Cys Leu Thr Thr Lys Thr Ser Leu Trp Arg Lys Asn Ala Asn
          900   905   910

Gly Gly Tyr Val Cys Asn Ala Cys Gly Leu Tyr Gln Lys Leu His Ser
    915   920   925

Thr Pro Arg Pro Leu Asn Ile Ile Lys Gln Asn Asn Gly Glu Gln Ile
    930   935   940

Ile Arg Arg Arg Thr Arg Lys Arg Leu Asn Pro Glu Ala Leu Gln Ala
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Glu Gln Leu Asn Lys Gln Gln Arg Gly Ser Asn Glu Glu Gln Val Asn
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Gly Ser Pro Leu Glu Arg Arg Ser Glu Asp His Leu Thr Glu Ser His
          980   985   990

Gln Arg Glu Ile Pro Leu Pro Ser Leu Ser Lys Tyr Glu Ala Gln Gly
    995   1000   1005

Ser Leu Thr Lys Ser His Ser Ala Gln Gln Pro Val Leu Val Ser Gln
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Thr Leu Asp Ile His Lys Arg Met Gln Pro Leu His Ile Gln Ile Lys
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Ser Pro Gln Glu Ser Thr Gly Asp Pro Gly Asn Ser Ser Ser Val Ser
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27

Glu Gly Lys Gly Ser Ser Glu Arg Gly Ser Pro Ile Glu Lys Tyr Met
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Arg Pro Ala Lys His Pro Asn Tyr Ser Pro Pro Gly Ser Pro Ile Glu
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Lys Tyr Gln Tyr Pro Leu Phe Gly Leu Pro Phe Val His Asn Asp Phe
   1090   1095   1100

Gln Ser Glu Ala Asp Trp Leu Arg Phe Trp Ser Lys Tyr Lys Leu Ser
1105   1110   1115   1120

Val Pro Gly Asn Pro His Tyr Leu Ser His Val Pro Gly Leu Pro Asn
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Pro Cys Gln Asn Tyr Val Pro Tyr Pro Thr Phe Asn Leu Pro Pro His
         1140   1145   1150

Phe Ser Ala Val Gly Ser Asp Asn Asp Ile Pro Leu Asp Leu Ala Ile
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Lys His Ser Arg Pro Gly Pro Thr Ala Asn Gly Ala Ser Lys Glu Lys
   1170   1175   1180

Thr Lys Ala Pro Pro Asn Val Lys Asn Glu Gly Pro Leu Asn Val Val
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Lys Thr Glu Lys Val Asp Arg Ser Thr Gln Asp Glu Leu Ser Thr Lys
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Cys Val His Cys Gly Ile Val Phe Leu Asp Glu Val Met Tyr Ala Leu
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His Met Ser Cys His Gly Asp Ser Gly Pro Phe Gln Cys Ser Ile Cys
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Gln His Leu Cys Thr Asp Lys Tyr Asp Phe Thr Thr His Ile Gln Arg
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Gly Leu His Arg Asn Asn Ala Gln Val Glu Lys Asn Gly Lys Pro Lys
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<210> 34
<211> 5277
<212> DNA
<213> Homo sapiens

28

<400> 34

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29

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<210> 35
<211> 871
<212> PRT
<213> Homo sapiens

<400> 35

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Leu Leu Gly Ser Leu Cys Ser Thr Val Arg Ser Pro Arg Phe Arg Gly
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Arg Ile Gln Gln Glu Arg Lys Asn Ile Arg Pro Asn Ile Ile Leu Val
        35              40              45

Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser Leu Gln Val Met Asn
        50              55              60

Lys Thr Arg Lys Ile Met Glu His Gly Gly Ala Thr Phe Ile Asn Ala
65              70              75              80

Phe Val Thr Thr Pro Met Cys Cys Pro Ser Arg Ser Ser Met Leu Thr
            85              90              95

Gly Lys Tyr Val His Asn His Asn Val Tyr Thr Asn Asn Glu Asn Cys
            100             105             110

Ser Ser Pro Ser Trp Gln Ala Met His Glu Pro Arg Thr Phe Ala Val
        115             120             125

Tyr Leu Asn Asn Thr Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu
    130             135             140

Asn Glu Tyr Asn Gly Ser Tyr Ile Pro Pro Gly Trp Arg Glu Trp Leu
145             150             155             160

Gly Leu Ile Lys Asn Ser Arg Phe Tyr Asn Tyr Thr Val Cys Arg Asn
            165             170             175

Gly Ile Lys Glu Lys His Gly Phe Asp Tyr Ala Lys Asp Tyr Phe Thr
            180             185             190

Asp Leu Ile Thr Asn Glu Ser Ile Asn Tyr Phe Lys Met Ser Lys Arg
        195             200             205

Met Tyr Pro His Arg Pro Val Met Met Val Ile Ser His Ala Ala Pro
    210             215             220

His Gly Pro Glu Asp Ser Ala Pro Gln Phe Ser Lys Leu Tyr Pro Asn
225             230             235             240

Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Met Asp
            245             250             255

Lys His Trp Ile Met Gln Tyr Thr Gly Pro Met Leu Pro Ile His Met
            260             265             270

Glu Phe Thr Asn Ile Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser
    275             280             285

Val Asp Asp Ser Val Glu Arg Leu Tyr Asn Met Leu Val Glu Thr Gly
    290             295             300
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31

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Glu Leu Glu Asn Thr Tyr Ile Ile Tyr Thr Ala Asp His Gly Tyr His
305                 310             315                     320

Ile Gly Gln Phe Gly Leu Val Lys Gly Lys Ser Met Pro Tyr Asp Phe
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Asp Ile Arg Val Pro Phe Phe Ile Arg Gly Pro Ser Val Glu Pro Gly
            340             345             350

Ser Ile Val Pro Gln Ile Val Leu Asn Ile Asp Leu Ala Pro Thr Ile
            355             360             365

Leu Asp Ile Ala Gly Leu Asp Thr Pro Pro Asp Val Asp Gly Lys Ser
    370             375             380

Val Leu Lys Leu Leu Asp Pro Glu Lys Pro Gly Asn Arg Phe Arg Thr
385             390             395                     400

Asn Lys Lys Ala Lys Ile Trp Arg Asp Thr Phe Leu Val Glu Arg Gly
            405             410             415

Lys Phe Leu Arg Lys Lys Glu Glu Ser Ser Lys Asn Ile Gln Gln Ser
            420             425             430

Asn His Leu Pro Lys Tyr Glu Arg Val Lys Glu Leu Cys Gln Gln Ala
        435             440             445

Arg Tyr Gln Thr Ala Cys Glu Gln Pro Gly Gln Lys Trp Gln Cys Ile
    450             455             460

Glu Asp Thr Ser Gly Lys Leu Arg Ile His Lys Cys Lys Gly Pro Ser
465             470             475                     480

Asp Leu Leu Thr Val Arg Gln Ser Thr Arg Asn Leu Tyr Ala Arg Gly
            485             490             495

Phe His Asp Lys Asp Lys Glu Cys Ser Cys Arg Glu Ser Gly Tyr Arg
        500             505             510

Ala Ser Arg Ser Gln Arg Lys Ser Gln Arg Gln Phe Leu Arg Asn Gln
    515             520             525

Gly Thr Pro Lys Tyr Lys Pro Arg Phe Val His Thr Arg Gln Thr Arg
    530             535             540

Ser Leu Ser Val Glu Phe Glu Gly Glu Ile Tyr Asp Ile Asn Leu Glu
545             550             555                     560

Glu Glu Glu Glu Leu Gln Val Leu Gln Pro Arg Asn Ile Ala Lys Arg
            565             570             575
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32

His Asp Glu Gly His Lys Gly Pro Arg Asp Leu Gln Ala Ser Ser Gly
          580   585   590

Gly Asn Arg Gly Arg Met Leu Ala Asp Ser Ser Asn Ala Val Gly Pro
     595   600   605

Pro Thr Thr Val Arg Val Thr His Lys Cys Phe Ile Leu Pro Asn Asp
610   615   620

Ser Ile His Cys Glu Arg Glu Leu Tyr Gln Ser Ala Arg Ala Trp Lys
625   630   635   640

Asp His Lys Ala Tyr Ile Asp Lys Glu Ile Glu Ala Leu Gln Asp Lys
          645   650   655

Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Arg Arg Lys Pro
          660   665   670

Glu Glu Cys Ser Cys Ser Lys Gln Ser Tyr Tyr Asn Lys Glu Lys Gly
     675   680   685

Val Lys Lys Gln Glu Lys Leu Lys Ser His Leu His Pro Phe Lys Glu
   690   695   700

Ala Ala Gln Glu Val Asp Ser Lys Leu Gln Leu Phe Lys Glu Asn Asn
705   710   715   720

Arg Arg Arg Lys Lys Glu Arg Lys Glu Lys Arg Arg Gln Arg Lys Gly
          725   730   735

Glu Glu Cys Ser Leu Pro Gly Leu Thr Cys Phe Thr His Asp Asn Asn
     740   745   750

His Trp Gln Thr Ala Pro Phe Trp Asn Leu Gly Ser Phe Cys Ala Cys
     755   760   765

Thr Ser Ser Asn Asn Asn Thr Tyr Trp Cys Leu Arg Thr Val Asn Glu
   770   775   780

Thr His Asn Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr
785   790   795   800

Phe Asp Met Asn Thr Asp Pro Tyr Gln Leu Thr Asn Thr Val His Thr
          805   810   815

Val Glu Arg Gly Ile Leu Asn Gln Leu His Val Gln Leu Met Glu Leu
          820   825   830

Arg Ser Cys Gln Gly Tyr Lys Gln Cys Asn Pro Arg Pro Lys Asn Leu
     835   840   845

33

Asp Val Gly Asn Lys Asp Gly Gly Ser Tyr Asp Leu His Arg Gly Gln
   850   855   860

Leu Trp Asp Gly Trp Glu Gly
865   870

<210> 36
<211> 1922
<212> DNA
<213> Homo sapiens

<400> 36
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<210> 37
<211> 1179
<212> DNA

34

<213> Homo sapiens

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<210> 38
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<212> PRT
<213> Homo sapiens

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<223> "Xaa" at position 111 can be any amino acid.

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             20   25   30

Ser Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile
         35   40   45

Leu Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr·Cys
     50   55   60

Glu Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu
 65   70   75   80

35

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Ala Trp Asn Met Ser Glu Cys Gly Gly Leu Cys Gln Pro Thr Glu Tyr
             85                  90                  95

Ser Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Xaa Phe
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Gln Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys Gly Gly Gly Leu
            115              120              125

Ala Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg
        130              135              140

Val Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr Thr His Arg Cys
145              150              155              160

Ile Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn
                165              170              175

Cys Val Ser Cys Pro Gly Asn Thr Thr Asp Phe Asp Gly Ser Thr
            180              185              190

Asn Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly Glu Leu Gly Asp
        195              200              205

Phe Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala
    210              215              220

Asn Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile
225              230              235              240

Leu Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly
                245              250              255

Asp Tyr Leu Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr
            260              265              270

Tyr Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg
        275              280              285

Ser Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala
    290              295              300

Arg Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu
305              310              315              320

Leu Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn
                325              330              335

His Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp
        340              345              350
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36

Val Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser
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Arg Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val
    370   375   380

Ser Arg Phe Leu Arg Pro Tyr Lys
385   390

<210> 39
<211> 392
<212> PRT
<213> Homo sapiens

<220>
<221> UNSURE
<222> (111)
<223> "Xaa" at position 111 can be any amino acid.

<400> 39
Met Asn Leu Asp Val Ala Lys Lys Pro Pro Arg Thr Ser Glu Arg Gln
  1   5   10   15

Ala Glu Ser Cys Gly Val Gly Gln Gly His Ala Glu Asn Gln Cys Val
             20   25   30

Ser Cys Arg Ala Gly Thr Tyr Tyr Asp Gly Ala Arg Glu Arg Cys Ile
         35   40   45

Leu Cys Pro Asn Gly Thr Phe Gln Asn Glu Glu Gly Gln Met Thr Cys
     50   55   60

Glu Pro Cys Pro Arg Pro Gly Asn Ser Gly Ala Leu Lys Thr Pro Glu
 65   70   75   80

Ala Trp Asn Met Ser Glu Cys Gly Gly Leu Cys Gln Pro Thr Glu Tyr
                 85   90   95

Ser Ala Asp Gly Phe Ala Pro Cys Gln Leu Cys Ala Leu Gly Xaa Phe
             100   105   110

Gln Pro Glu Ala Gly Arg Thr Ser Cys Phe Pro Cys Gly Gly Gly Leu
         115   120   125

Ala Thr Lys His Gln Gly Ala Thr Ser Phe Gln Asp Cys Glu Thr Arg
         130   135   140

Val Gln Cys Ser Pro Gly His Phe Tyr Asn Thr Thr Thr His Arg Cys
145   150   155   160

37

Ile Arg Cys Pro Val Gly Thr Tyr Gln Pro Glu Phe Gly Lys Asn Asn
                165   170   175

Cys Val Ser Cys Pro Gly Asn Thr Thr Thr Asp Phe Asp Gly Ser Thr
                180   185   190

Asn Ile Thr Gln Cys Lys Asn Arg Arg Cys Gly Gly Glu Leu Gly Asp
            195   200   205

Phe Thr Gly Tyr Ile Glu Ser Pro Asn Tyr Pro Gly Asn Tyr Pro Ala
        210   215   220

Asn Thr Glu Cys Thr Trp Thr Ile Asn Pro Pro Pro Lys Arg Arg Ile
225   230   235   240

Leu Ile Val Val Pro Glu Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly
                245   250   255

Asp Tyr Leu Val Met Arg Lys Thr Ser Ser Ser Asn Ser Val Thr Thr
                260   265   270

Tyr Glu Thr Cys Gln Thr Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg
        275   280   285

Ser Lys Lys Leu Trp Ile Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala
    290   295   300

Arg Gly Phe Gln Val Pro Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu
305   310   315   320

Leu Ile Glu Asp Ile Val Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn
            325   330   335

His Gln Glu Ile Leu Lys Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp
            340   345   350

Val Leu Ala His Pro Gln Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser
        355   360   365

Arg Glu Met Phe Pro Arg Ser Phe Ile Arg Leu Leu Arg Ser Lys Val
    370   375   380

Ser Arg Phe Leu Arg Pro Tyr Lys
385   390

<210> 40
<211> 162
<212> PRT
<213> Mouse

38

<400> 40

Thr	Ile	Asn	Pro	Pro	Pro	Lys	Arg	Arg	Ile	Leu	Ile	Val	Val	Pro	Glu
1				5					10					15	

Ile Phe Leu Pro Ile Glu Asp Asp Cys Gly Asp Tyr Leu Val Met Arg
            20   25   30

Lys Thr Ser Ser Ser Asn Ser Val Thr Thr Tyr Glu Thr Cys Gln Thr
        35   40   45

Tyr Glu Arg Pro Ile Ala Phe Thr Ser Arg Ser Lys Lys Leu Trp Ile
    50   55   60

Gln Phe Lys Ser Asn Glu Gly Asn Ser Ala Arg Gly Phe Gln Val Pro
65   70   75   80

Tyr Val Thr Tyr Asp Glu Asp Tyr Gln Glu Leu Ile Glu Asp Ile Val
            85   90   95

Arg Asp Gly Arg Leu Tyr Ala Ser Glu Asn His Gln Glu Ile Leu Lys
            100   105   110

Asp Lys Lys Leu Ile Lys Ala Leu Phe Asp Val Leu Ala His Pro Gln
    115   120   125

Asn Tyr Phe Lys Tyr Thr Ala Gln Glu Ser Arg Glu Met Phe Pro Arg
    130   135   140

Ser Phe Ile Arg Leu Leu Arg Ser Lys Val Ser Arg Phe Leu Arg Pro
145   150   155   160

Tyr Lys

<210> 41
<211> 2840
<212> DNA
<213> Homo sapiens

<400> 41
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cgactggagt ttggggggaag aaactctcct gcgccccaga agatttcttc ctcggcgaag 180
ggacagcgaa agatgagggt ggcaggaaga gaaggcgctt tctgtctgcc ggggtcgcag 240
cgcgagaggg cagtgccatg ttcctctcca tcctagtggc gctgtgcctg tggctgcacc 300
tggcgctggg cgtgcgcggc gcgccctgcg aggcggtgcg catccctatg tgccggcaca 360
tgccctggaa catcacgcgg atgcccaacc acctgcacca cagcacgcag agaacgcca 420
tcctggccat cgagcagtac gaggagctgg tggacgtgaa ctgcagcgcc gtgctgcgct 480
tcttcttctg tgccatgtac gcgcccattt gcaccctgga gttcctgcac gaccctatca 540
agccgtgcaa gtcggtgtgc caacgcgcgc gcgacgactg cgagcccctc atgaagatgt 600
```

```
acaaccacag ctggcccgaa agcctggcct gcgacgagct gcctgtctat gaccgtggcg 660
tgtgcatttc gcctgaagcc atcgtcacgg acctcccgga ggatgttaag tggatagaca 720
tcacaccaga catgatggta caggaaaggc ctcttgatgt tgactgtaaa cgcctaagcc 780
ccgatcggtg caagtgtaaa aaggtgaagc caactttggc aacgtatctc agcaaaaact 840
acagctatgt tattcatgcc aaaataaaag ctgtgcagag gagtggctgc aatgaggtca 900
caacggtggt ggatgtaaaa gagatcttca agtcctcatc acccatccct cgaactcaag 960
tcccgctcat tacaaattct tcttgccagt gtccacacat cctgccccat caagatgttc 1020
tcatcatgtg ttacgagtgg cgttcaagga tgatgcttct tgaaaattgc ttagttgaaa 1080
aatggagaga tcagcttagt aaaagatcca tacagtggga agagaggctg caggaacagc 1140
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tgccctttgg tacagaaggt gagttaaagc tggtggaaaa ggcttattgc attgcattca 1560
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tatgttttat tacctttga tatctgttgt tgcaatgtta gtgatgtttt aaaatgtgat 1740
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gtttatggtc tgcagaagga tttttgtgat gaaaggggat tttttgaaaa attagagaag 1860
tagcatatgg aaaattataa tgtgttttt taccaatgac ttcagtttct gtttttagct 1920
agaaacttaa aaacaaaaat aataataaag aaaaataaat aaaaaggaga ggcagacaat 1980
gtctggattc ctgttttttg gttacctgat ttccatgatc atgatgcttc ttgtcaacac 2040
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tagttggcta atgctcaagt attttatacc cacaagagag gtatgtcact catcttactt 2160
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ttgggatact ttaatcagaa aaaagaact tatttgcagc attttatcaa caaatttcat 2400
aattgtggac aattggaggc atttatttta aaaaacaatt ttattggcct tttgctaaca 2460
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cctatctaat cctactctcc actacacaga ggtaatcact attagtattt tggcatatta 2580
ttctccaggt gtttgcttat gcacttataa aatgatttga acaaataaaa ctaggaacct 2640
gtatacatgt gtttcataac ctgcctcctt tgcttggccc tttattgaga taagttttcc 2700
tgtcaagaaa gcagaaacca tctcatttct aacagctgtg ttatattcca tagtatgcat 2760
tactcaacaa actgttgtgc tattggatac ttaggtggtt tcttcactga caatactgaa 2820
taaacatctc accggaattc                                           2840
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<210> 42
<211> 1041
<212> DNA
<213> Homo sapiens

<400> 42
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ggcgcgccct gcgaggcggt gcgcatccct atgtgccggc acatgccctg gaacatcacg 120
cggatgccca accacctgca ccacagcacg caggagaacg ccatcctggc catcgagcag 180
tacgaggagc tggtggacgt gaactgcagc gccgtgctgc gcttcttctt ctgtgccatg 240
tacgcgccca tttgcaccct ggagttcctg cacgaccta tcaagccgtg caagtcggtg 300
```
```
                                    40
```

```
tgccaacgcg cgcgcgacga ctgcgagccc ctcatgaaga tgtacaacca cagctggccc 360
gaaagcctgg cctgcgacga gctgcctgtc tatgaccgtg gcgtgtgcat ttcgcctgaa 420
gccatcgtca cggacctccc ggaggatgtt aagtggatag acatcacacc agacatgatg 480
gtacaggaaa ggcctcttga tgttgactgt aaacgcctaa gccccgatcg gtgcaagtgt 540
aaaaaggtga agccaacttt ggcaacgtat ctcagcaaaa actacagcta tgttattcat 600
gccaaaataa aagctgtgca gaggagtggc tgcaatgagg tcacaacggt ggtggatgta 660
aaagagatct tcaagtcctc atcacccatc cctcgaactc aagtcccgct cattacaaat 720
tcttcttgcc agtgtccaca catcctgccc catcaagatg ttctcatcat gtgttacgag 780
tggcgttcaa ggatgatgct tcttgaaaat tgcttagttg aaaaatggag agatcagctt 840
agtaaaagat ccatacagtg ggaagagagg ctgcaggaac agcggagaac agttcaggac 900
aagaagaaaa cagccgggcg caccagtcgt agtaatcccc ccaaaccaaa gggaaagcct 960
cctgctccca aaccagccag tcccaagaag aacattaaaa ctaggagtgc ccagaagaga 1020
acaaacccga aaagagtgtg a                                       1041


<210> 43
<211> 346
<212> PRT
<213> Homo sapiens

<400> 43
Met Phe Leu Ser Ile Leu Val Ala Leu Cys Leu Trp Leu His Leu Ala
  1               5                  10                  15

Leu Gly Val Arg Gly Ala Pro Cys Glu Ala Val Arg Ile Pro Met Cys
                 20                  25                  30

Arg His Met Pro Trp Asn Ile Thr Arg Met Pro Asn His Leu His His
             35                  40                  45

Ser Thr Gln Glu Asn Ala Ile Leu Ala Ile Glu Gln Tyr Glu Glu Leu
         50                  55                  60

Val Asp Val Asn Cys Ser Ala Val Leu Arg Phe Phe Phe Cys Ala Met
 65                  70                  75                  80

Tyr Ala Pro Ile Cys Thr Leu Glu Phe Leu His Asp Pro Ile Lys Pro
                 85                  90                  95

Cys Lys Ser Val Cys Gln Arg Ala Arg Asp Asp Cys Glu Pro Leu Met
                100                 105                 110

Lys Met Tyr Asn His Ser Trp Pro Glu Ser Leu Ala Cys Asp Glu Leu
             115                 120                 125

Pro Val Tyr Asp Arg Gly Val Cys Ile Ser Pro Glu Ala Ile Val Thr
         130                 135                 140

Asp Leu Pro Glu Asp Val Lys Trp Ile Asp Ile Thr Pro Asp Met Met
145                 150                 155                 160
```

41

```
Val Gln Glu Arg Pro Leu Asp Val Asp Cys Lys Arg Leu Ser Pro Asp
            165                 170                 175

Arg Cys Lys Cys Lys Lys Val Lys Pro Thr Leu Ala Thr Tyr Leu Ser
            180                 185                 190

Lys Asn Tyr Ser Tyr Val Ile His Ala Lys Ile Lys Ala Val Gln Arg
            195                 200                 205

Ser Gly Cys Asn Glu Val Thr Thr Val Val Asp Val Lys Glu Ile Phe
    210                 215                 220

Lys Ser Ser Ser Pro Ile Pro Arg Thr Gln Val Pro Leu Ile Thr Asn
225                 230                 235                 240

Ser Ser Cys Gln Cys Pro His Ile Leu Pro His Gln Asp Val Leu Ile
            245                 250                 255

Met Cys Tyr Glu Trp Arg Ser Arg Met Met Leu Leu Glu Asn Cys Leu
            260                 265                 270

Val Glu Lys Trp Arg Asp Gln Leu Ser Lys Arg Ser Ile Gln Trp Glu
            275                 280                 285

Glu Arg Leu Gln Glu Gln Arg Arg Thr Val Gln Asp Lys Lys Lys Thr
            290                 295                 300

Ala Gly Arg Thr Ser Arg Ser Asn Pro Pro Lys Pro Lys Gly Lys Pro
305                 310                 315                 320

Pro Ala Pro Lys Pro Ala Ser Pro Lys Lys Asn Ile Lys Thr Arg Ser
            325                 330                 335

Ala Gln Lys Arg Thr Asn Pro Lys Arg Val
            340                 345


<210> 44
<211> 749
<212> DNA
<213> Homo sapiens

<400> 44
cggcaccaag agcactggcc aagtcagctt cttctgagag agtctctaga agacatgatg 60
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gcaataaaaa aggaaaagag gcctcctcag acactctcaa gaggatgggg agatgacatc 180
acttgggtac aaacttatga agaaggtctc ttttatgctc aaaaaagtaa gaagccatta 240
atggttattc atcacctgga ggattgtcaa tactctcaag cactaaagaa agtatttgcc 300
caaaatgaag aaatacaaga aatggctcag aataagttca tcatgctaaa ccttatgcat 360
gaaaccactg ataagaattt atcacctgat gggcaatatg tgcctagaat catgtttgta 420
gacccttctt taacagttag agctgacata gctggaagat actctaacag attgtacaca 480
```

42

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tatgagcctc gggatttacc cctattgata gaaaacatga agaaagcatt aagacttatt 540
cagtcagagc tataagagat gatagaaaaa agccttcact tcaaagaagt caaatttcat 600
gaagaaaacc tctggcacat tgacaaatac taaatgtgca agtatataga ttttgtaata 660
ttactattta gttttttaa tgtgtttgca atagtcttat taaataaat gttttttaaa 720
tctgaaaaaa aaaaaaaaa aaaaaaaa                                    749
```

<210> 45
<211> 501
<212> DNA
<213> Homo sapiens

<400> 45
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gccattgcaa taaaaaagga aaagaggcct cctcagacac tctcaagagg atggggagat 120
gacatcactt gggtacaaac ttatgaagaa ggtctctttt atgctcaaaa aagtaagaag 180
ccattaatgg ttattcatca cctggaggat tgtcaatact ctcaagcact aaagaaagta 240
tttgcccaaa atgaagaaat acaagaaatg gctcagaata agttcatcat gctaaacctt 300
atgcatgaaa ccactgataa gaattatca cctgatgggc aatatgtgcc tagaatcatg 360
tttgtagacc cttctttaac agttagagct gacatagctg gaagatactc taacagattg 420
tacacatatg agcctcggga tttacccta ttgatagaaa acatgaagaa agcattaaga 480
cttattcagt cagagctata a                                          501
```

<210> 46
<211> 166
<212> PRT
<213> Homo sapiens

<400> 46
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Met Met Leu His Ser Ala Leu Gly Leu Cys Leu Leu Leu Val Thr Val
 1               5                  10                  15

Ser Ser Asn Leu Ala Ile Ala Ile Lys Lys Glu Lys Arg Pro Pro Gln
            20                  25                  30

Thr Leu Ser Arg Gly Trp Gly Asp Asp Ile Thr Trp Val Gln Thr Tyr
        35                  40                  45

Glu Glu Gly Leu Phe Tyr Ala Gln Lys Ser Lys Lys Pro Leu Met Val
    50                  55                  60

Ile His His Leu Glu Asp Cys Gln Tyr Ser Gln Ala Leu Lys Lys Val
65                  70                  75                  80

Phe Ala Gln Asn Glu Glu Ile Gln Glu Met Ala Gln Asn Lys Phe Ile
                85                  90                  95

Met Leu Asn Leu Met His Glu Thr Thr Asp Lys Asn Leu Ser Pro Asp
               100                 105                 110
```

43

Gly Gln Tyr Val Pro Arg Ile Met Phe Val Asp Pro Ser Leu Thr Val
        115   120   125

Arg Ala Asp Ile Ala Gly Arg Tyr Ser Asn Arg Leu Tyr Thr Tyr Glu
        130   135   140

Pro Arg Asp Leu Pro Leu Leu Ile Glu Asn Met Lys Lys Ala Leu Arg
145   150   155   160

Leu Ile Gln Ser Glu Leu
                165

<210> 47
<211> 3493
<212> DNA
<213> Homo sapiens

<400> 47
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cgctgccgag gcgcccgggg acccgcaggc ggccgcgtcc ttgctggccc ctatggacgt 180
gggggaggag ccgctggaga aggcggcgcg cgcccgcact gccaaggacc ccaacaccta 240
taaagtactc tcgctggtat tgtcagtatg tgtgttaaca acaatacttg gttgtatatt 300
tgggttgaaa ccaagctgtg ccaaagaagt taaaagttgc aaaggtcgct gtttcgagag 360
aacatttggg aactgtcgct gtgatgctgc ctgtgttgag cttggaaact gctgtttaga 420
ttaccaggag acgtgcatag aaccagaaca tatatggact tgcaacaaat tcaggtgtgg 480
tgagaaaagg ttgaccagaa gcctctgtgc ctgttcagat gactgcaagg acaagggcga 540
ctgctgcatc aactacagtt ctgtgtgtca aggtgagaaa agttgggtag aagaaccatg 600
tgagagcatt aatgagccac agtgcccagc agggtttgaa acgcctccta ccctcttatt 660
ttctttggat ggattcaggg cagaatattt acacacttgg ggtggacttc ttcctgttat 720
tagcaaacta aaaaaatgtg gaacatatac taaaaacatg agaccggtat atccaacaaa 780
aactttcccc aatcactaca gcattgtcac cggattgtat ccagaatctc atggcataat 840
cgacaataaa atgtatgatc ccaaaatgaa tgcttccttt tcacttaaaa gtaaagagaa 900
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caagtctggc acatttttct ggccaggatc agatgtggaa attaacggaa ttttcccaga 1020
catctataaa atgtataatg gttcagtacc atttgaagaa aggattttag ctgttcttca 1080
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acctaagcgt ttgcactttg ctaagagtga tagaattgag cccttgacat tctatttgga 1560
ccctcagtgg caacttgcat tgaatccctc agaaaggaaa tattgtggaa gtggatttca 1620
tggctctgac aatgtatttt caaatatgca agccctcttt gttggctatg gacctggatt 1680
caagcatggc attgaggctg acacctttga aaacattgaa gtctataact taatgtgtga 1740
tttactgaat ttgacaccgg ctcctaataa cggaactcat ggaagtctta accaccttct 1800
aaagaatcct gtttatacgc caaagcatcc caaagaagtg caccccctgg tacagtgccc 1860
cttcacaaga aaccccagag ataaccttgg ctgctcatgt aacccttcga ttttgccgat 1920

44

```
tgaggatttt caaacacagt tcaatctgac tgtggcagaa gagaagatta ttaagcatga 1980
aactttaccc tatggaagac ctagagttct ccagaaggaa aacaccatct gtcttctttc 2040
ccagcaccag tttatgagtg gatacagcca agacatctta atgccccttt ggacatccta 2100
taccgtggac agaaatgaca gtttctctac ggaagacttc tccaactgtc tgtaccagga 2160
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ctttcatgac accctactgc gaaagtatgc tgaagaaaga aatggtgtca atgtcgtcag 2400
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ttaatcttat gtgttttctt tttaattttt tgattggatt tctttagatt taatggttca 3420
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<210> 48
<211> 925
<212> PRT
<213> Homo sapiens

<400> 48

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Met Glu Arg Asp Gly Cys Ala Gly Gly Ser Arg Gly Gly Glu Gly
 1               5                  10                  15


Gly Arg Ala Pro Arg Glu Gly Pro Ala Gly Asn Gly Arg Asp Arg Gly
            20                  25                  30


Arg Ser His Ala Ala Glu Ala Pro Gly Asp Pro Gln Ala Ala Ala Ser
        35                  40                  45


Leu Leu Ala Pro Met Asp Val Gly Glu Glu Pro Leu Glu Lys Ala Ala
    50                  55                  60


Arg Ala Arg Thr Ala Lys Asp Pro Asn Thr Tyr Lys Val Leu Ser Leu
65                  70                  75                  80


Val Leu Ser Val Cys Val Leu Thr Thr Ile Leu Gly Cys Ile Phe Gly
```

45

Leu Lys Pro Ser Cys Ala Lys Glu Val Lys Ser Cys Lys Gly Arg Cys
        100   105   110

Phe Glu Arg Thr Phe Gly Asn Cys Arg Cys Asp Ala Ala Cys Val Glu
        115   120   125

Leu Gly Asn Cys Cys Leu Asp Tyr Gln Glu Thr Cys Ile Glu Pro Glu
    130   135   140

His Ile Trp Thr Cys Asn Lys Phe Arg Cys Gly Glu Lys Arg Leu Thr
145   150   155   160

Arg Ser Leu Cys Ala Cys Ser Asp Asp Cys Lys Asp Lys Gly Asp Cys
            165   170   175

Cys Ile Asn Tyr Ser Ser Val Cys Gln Gly Glu Lys Ser Trp Val Glu
            180   185   190

Glu Pro Cys Glu Ser Ile Asn Glu Pro Gln Cys Pro Ala Gly Phe Glu
        195   200   205

Thr Pro Pro Thr Leu Leu Phe Ser Leu Asp Gly Phe Arg Ala Glu Tyr
    210   215   220

Leu His Thr Trp Gly Gly Leu Leu Pro Val Ile Ser Lys Leu Lys Lys
225   230   235   240

Cys Gly Thr Tyr Thr Lys Asn Met Arg Pro Val Tyr Pro Thr Lys Thr
            245   250   255

Phe Pro Asn His Tyr Ser Ile Val Thr Gly Leu Tyr Pro Glu Ser His
            260   265   270

Gly Ile Ile Asp Asn Lys Met Tyr Asp Pro Lys Met Asn Ala Ser Phe
        275   280   285

Ser Leu Lys Ser Lys Glu Lys Phe Asn Pro Glu Trp Tyr Lys Gly Glu
    290   295   300

Pro Ile Trp Val Thr Ala Lys Tyr Gln Gly Leu Lys Ser Gly Thr Phe
305   310   315   320

Phe Trp Pro Gly Ser Asp Val Glu Ile Asn Gly Ile Phe Pro Asp Ile
            325   330   335

Tyr Lys Met Tyr Asn Gly Ser Val Pro Phe Glu Glu Arg Ile Leu Ala
        340   345   350

Val Leu Gln Trp Leu Gln Leu Pro Lys Asp Glu Arg Pro His Phe Tyr

46

Thr Leu Tyr Leu Glu Glu Pro Asp Ser Ser Gly His Ser Tyr Gly Pro
   370   375   380

Val Ser Ser Glu Val Ile Lys Ala Leu Gln Arg Val Asp Gly Met Val
385   390   395   400

Gly Met Leu Met Asp Gly Leu Lys Glu Leu Asn Leu His Arg Cys Leu
          405   410   415

Asn Leu Ile Leu Ile Ser Asp His Gly Met Glu Gln Gly Ser Cys Lys
          420   425   430

Lys Tyr Ile Tyr Leu Asn Lys Tyr Leu Gly Asp Val Lys Asn Ile Lys
          435   440   445

Val Ile Tyr Gly Pro Ala Ala Arg Leu Arg Pro Ser Asp Val Pro Asp
     450   455   460

Lys Tyr Tyr Ser Phe Asn Tyr Glu Gly Ile Ala Arg Asn Leu Ser Cys
465   470   475   480

Arg Glu Pro Asn Gln His Phe Lys Pro Tyr Leu Lys His Phe Leu Pro
          485   490   495

Lys Arg Leu His Phe Ala Lys Ser Asp Arg Ile Glu Pro Leu Thr Phe
          500   505   510

Tyr Leu Asp Pro Gln Trp Gln Leu Ala Leu Asn Pro Ser Glu Arg Lys
          515   520   525

Tyr Cys Gly Ser Gly Phe His Gly Ser Asp Asn Val Phe Ser Asn Met
     530   535   540

Gln Ala Leu Phe Val Gly Tyr Gly Pro Gly Phe Lys His Gly Ile Glu
545   550   555   560

Ala Asp Thr Phe Glu Asn Ile Glu Val Tyr Asn Leu Met Cys Asp Leu
          565   570   575

Leu Asn Leu Thr Pro Ala Pro Asn Asn Gly Thr His Gly Ser Leu Asn
          580   585   590

His Leu Leu Lys Asn Pro Val Tyr Thr Pro Lys His Pro Lys Glu Val
          595   600   605

His Pro Leu Val Gln Cys Pro Phe Thr Arg Asn Pro Arg Asp Asn Leu
          610   615   620

Gly Cys Ser Cys Asn Pro Ser Ile Leu Pro Ile Glu Asp Phe Gln Thr

47

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        625                    630                    635                    640

Gln Phe Asn Leu Thr Val Ala Glu Glu Lys Ile Ile Lys His Glu Thr
                645                    650                    655

Leu Pro Tyr Gly Arg Pro Arg Val Leu Gln Lys Glu Asn Thr Ile Cys
                660                    665                    670

Leu Leu Ser Gln His Gln Phe Met Ser Gly Tyr Ser Gln Asp Ile Leu
                675                    680                    685

Met Pro Leu Trp Thr Ser Tyr Thr Val Asp Arg Asn Asp Ser Phe Ser
    690                    695                    700

Thr Glu Asp Phe Ser Asn Cys Leu Tyr Gln Asp Phe Arg Ile Pro Leu
705                    710                    715                    720

Ser Pro Val His Lys Cys Ser Phe Tyr Lys Asn Asn Thr Lys Val Ser
                725                    730                    735

Tyr Gly Phe Leu Ser Pro Pro Gln Leu Asn Lys Asn Ser Ser Gly Ile
                740                    745                    750

Tyr Ser Glu Ala Leu Leu Thr Thr Asn Ile Val Pro Met Tyr Gln Ser
                755                    760                    765

Phe Gln Val Ile Trp Arg Tyr Phe His Asp Thr Leu Leu Arg Lys Tyr
    770                    775                    780

Ala Glu Glu Arg Asn Gly Val Asn Val Val Ser Gly Pro Val Phe Asp
785                    790                    795                    800

Phe Asp Tyr Asp Gly Arg Cys Asp Ser Leu Glu Asn Leu Arg Gln Lys
                805                    810                    815

Arg Arg Val Ile Arg Asn Gln Glu Ile Leu Ile Pro Thr His Phe Phe
                820                    825                    830

Ile Val Leu Thr Ser Cys Lys Asp Thr Ser Gln Thr Pro Leu His Cys
                835                    840                    845

Glu Asn Leu Asp Thr Leu Ala Phe Ile Leu Pro His Arg Thr Asp Asn
    850                    855                    860

Ser Glu Ser Cys Val His Gly Lys His Asp Ser Ser Trp Val Glu Glu
865                    870                    875                    880

Leu Leu Met Leu His Arg Ala Arg Ile Thr Asp Val Glu His Ile Thr
                885                    890                    895

Gly Leu Ser Phe Tyr Gln Gln Arg Lys Glu Pro Val Ser Asp Ile Leu
```

48

900   905   910

Lys Leu Lys Thr His Leu Pro Thr Phe Ser Gln Glu Asp
        915   920   925

<210> 49
<211> 2709
<212> DNA
<213> Homo sapiens

<400> 49
ggttttcaaa tggaacattt tgatgcatca cttagtacct atttcaaggc attgctaggc 60
cctcgagata ctagagtaaa aggatggttt cttctggaca attatatacc cacatttatc 120
tgctctgtca tatatttact aattgtatgg ctgggaccaa aatacatgag gaataaacag 180
ccattctctt gccggggggat tttagtggtg tataaccttg gactcacact gctgtctctg 240
tatatgttct gtgagttagt aacaggagta tgggaaggca aatacaactt cttctgtcag 300
ggcacacgca ccgcaggaga atcagatatg aagattatcc gtgtcctctg gtggtactac 360
ttctccaaac tcatagaatt tatggacact ttcttcttca tcctgcgcaa gaacaaccac 420
cagatcacgg tcctgcacgt ctaccaccat gcctcgatgc tgaacatctg gtggtttgtg 480
atgaactggg tcccctgcgg ccactcttat tttggtgcca cacttaatag cttcatccac 540
gtcctcatgt actcttacta tggtttgtcg tcagtccctt ccatgcgtcc atacctctgg 600
tggaagaagt acatcactca ggggcagctg cttcagtttg tgctgacaat catccagacc 660
agctgcgggg tcatctggcc gtgcacattc cctcttggtt ggttgtattt ccagattgga 720
tacatgattt ccctgattgc tctcttcaca aacttctaca ttcagaccta caacaagaaa 780
ggggcctccc gaaggaaaga ccacctgaag gaccaccaga tgggtccat ggctgctgtg 840
aatggacaca ccaacagctt ttcacccctg gaaaacaatg tgaagccaag gaagctgcgg 900
aaggattgaa gtcaaagaat tgaaaccctc caaaccacgt catctgattg taagcacaat 960
atgagttgtg ccccaatgct cgttaacagc tgctgtaact agtctggcct acaatagtgt 1020
gattcatgta ggacttcttt catcaattca aaaccctag aaaacgtata cagattatat 1080
aagtagggat aagatttcta acatttctgg gctctctgac ccctgcgcta gactgtggaa 1140
agggagtatt attatagtat acaacactgc tgttgcctta ttagttataa catgataggt 1200
gctgaattgt gattcacaat ttaaaaacac tgtaatccaa actttttttt ttaactgtag 1260
atcatgcatg tgattgtaaa tgtaaatttg tacaatgttg ttatggtaga gaaacacaca 1320
tgccttaaaa tttaaaaagc agggcccaaa gcttattagt ttaaattagg gtatgtttca 1380
agtttgtatt aatttgtaat agctctgttt agaaaaaatc aaagaccatg atttatgaaa 1440
ctaatgtgac ataatttcca gtgacttgtt gatgtgaaat cagacacggc accttcagtt 1500
ttgtactatt ggctttgaat caagcaggct caaatctagt ggaacagtca gtttaacttt 1560
ttaacagatc ttatttttttt attttgagtg ccactattaa tgtaaaaagg ggggggctct 1620
acagcagtcg tgatgaaact taaatatata ttctttgtcc tcgagatttt aggaagggtg 1680
tagggtgagt aggccatttt taatttctga agtgctaagt gtttttatac agcaaacaaa 1740
aagtcaattt tgctttccac cagtgcgaga gaggatgtat acttttcaag agagatgatt 1800
gcctatttac cgtttgacag agtcccgtag atgagcaatg gggaactggt gccagggtc 1860
taaatttgga ttgatttatg cactgttatc tgttttgaca cagatttcct tgtaaaatgt 1920
gcctagttta ccaaaattaa caaaggggggg gaaaggacct tagaacttttt taaggtaaaa 1980
tcaaatatag ctacagcata agagaatcga gaaatttgat agaggtaact tgtttaatgt 2040
aaatctaata gtacttgtaa tttctttctg cttagaatct aaagatgtgt ttagaacctc 2100
ttgtttaaaa ataatagact gcttatcata aaatcacatc tcacacattt gaggcagtgg 2160
tcaaacaggt aaagcctatg atgtgtgtca ttttaaagtg tcggaattta gcctctgaat 2220
accttctcca ttggggggaaa gatattcttg gaaccactca tgacatatct tagaaggtca 2280
ttgacaatgt ataaactaat tgttggtttg atatttatgt aaatatcagt ttaccatgct 2340

49

```
ttaattttgc acattcgtac tatagggagc ctattggttc tctattagtc ttgtgggttt 2400
tctgtttgaa aaggagtcat ggcatctgtt tacatttacc ttatcaaacc tagaatgtgt 2460
atatttataa atgtatgtct tcattgctag gtactaattt gcagatgtct ttacatattt 2520
caatacagaa actataacat tcaatagtgt gctgtcaaag tgtgcttagc tcacctggat 2580
atacctacat tgttaaatgt ctaaacagta atcattaaaa cattttttgat taaaaaaaaa 2640
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2700
aaaaaaaaa                                                          2709
```

<210> 50
<211> 299
<212> PRT
<213> Homo sapiens

<400> 50

```
Met Glu His Phe Asp Ala Ser Leu Ser Thr Tyr Phe Lys Ala Leu Leu
 1               5                  10                  15

Gly Pro Arg Asp Thr Arg Val Lys Gly Trp Phe Leu Leu Asp Asn Tyr
            20                  25                  30

Ile Pro Thr Phe Ile Cys Ser Val Ile Tyr Leu Leu Ile Val Trp Leu
        35                  40                  45

Gly Pro Lys Tyr Met Arg Asn Lys Gln Pro Phe Ser Cys Arg Gly Ile
    50                  55                  60

Leu Val Val Tyr Asn Leu Gly Leu Thr Leu Leu Ser Leu Tyr Met Phe
65                  70                  75                  80

Cys Glu Leu Val Thr Gly Val Trp Glu Gly Lys Tyr Asn Phe Phe Cys
                85                  90                  95

Gln Gly Thr Arg Thr Ala Gly Glu Ser Asp Met Lys Ile Ile Arg Val
            100                 105                 110

Leu Trp Trp Tyr Tyr Phe Ser Lys Leu Ile Glu Phe Met Asp Thr Phe
    115                 120                 125

Phe Phe Ile Leu Arg Lys Asn Asn His Gln Ile Thr Val Leu His Val
    130                 135                 140

Tyr His His Ala Ser Met Leu Asn Ile Trp Trp Phe Val Met Asn Trp
145                 150                 155                 160

Val Pro Cys Gly His Ser Tyr Phe Gly Ala Thr Leu Asn Ser Phe Ile
                165                 170                 175

His Val Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Ser Val Pro Ser Met
                180                 185                 190
```

50

```
Arg Pro Tyr Leu Trp Trp Lys Lys Tyr Ile Thr Gln Gly Gln Leu Leu
        195             200             205

Gln Phe Val Leu Thr Ile Ile Gln Thr Ser Cys Gly Val Ile Trp Pro
        210             215             220

Cys Thr Phe Pro Leu Gly Trp Leu Tyr Phe Gln Ile Gly Tyr Met Ile
225                 230             235                 240

Ser Leu Ile Ala Leu Phe Thr Asn Phe Tyr Ile Gln Thr Tyr Asn Lys
                245             250             255

Lys Gly Ala Ser Arg Arg Lys Asp His Leu Lys Asp His Gln Asn Gly
                260             265             270

Ser Met Ala Ala Val Asn Gly His Thr Asn Ser Phe Ser Pro Leu Glu
                275             280             285

Asn Asn Val Lys Pro Arg Lys Leu Arg Lys Asp
        290             295
```

```
<210> 51
<211> 1019
<212> DNA
<213> Homo sapiens

<400> 51
ttttttttta aacaaacaaa tgcgggttta tttctcagat gatgttcatc cgtgaatggt 60
ccagggaagg acctttcacc ttgactatat ggcattatgt catcacaagc tctgaggctt 120
ctcctttcca tcctgcgtgg acagctaaga cctcagtttt caatagcatc tagagcagtg 180
ggactcagct ggggtgattt cgcccccat ctccgggggga atgtctgaag caattttgg 240
ttacctcaat gagggagtgg aggaggatac agtgctacta ccaactagtg gataaaggcc 300
agggatgctg ctcaacctcc taccatgtac aggacgtctc cccattacaa ctacccaatc 360
cgaagtgtca actgtgtcag gactaagaaa ccctggtttt gagtagaaaa gggcctggaa 420
agaggggagc caacaaatct gtctgcttcc tcacattagt cattggcaaa taagcattct 480
gtctctttgg ctgctgcctc agcacagaga gccagaactc tatcgggcac caggataaca 540
tctctcagtg aacagagttg acaaggccta tgggaaatgc ctgatgggat tatcttcagc 600
ttgttgagct tctaagtttc tttcccttca ttctaccctg caagccaagt tctgtaagag 660
aaatgcctga gttctagctc aggtttcttt actctgaatt tagatctcca gacccttcct 720
ggccacaatt caaattaagg caacaaacat ataccttcca tgaagcacac acagactttt 780
gaaagcaagg acaatgactg cttgaattga ggccttgagg aatgaagctt tgaaggaaaa 840
gaatactttg tttccagccc ccttcccaca ctcttcatgt gttaaccact gccttcctgg 900
accttggagc cacggtgact gtattacatg ttgttataga aaactgattt tagagttctg 960
atcgttcaag agaatgatta aatatacatt tcctacamaa aaaaaaaaa aagtcgacg 1019
```

```
<210> 52
<211> 1332
<212> DNA
<213> Homo sapiens
```

<400> 52
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agagatgggg gtctcactat gttgcccagg ctggtctcaa actcctgggc tcaagcgatc 60
ctttggcctc ggcctcccaa agtgcatgag ccaccatgcc tggcctgttt agttttgttt 120
caagttgaaa tacctttctt gtgtttcta attagaaaag taatatctac tcattgtaaa 180
aactcaaaca gtgcagaaat gtagaaagta gaaagtgtaa gtccctggtt gtcccttctg 240
cctgagcaca accactgctc acagtttgat gtatatcctt ccagagactc tcaaatttaa 300
gcaaataatt tttattacca tgtcttttta tttgaagacg tacatttgcc tccaaagttc 360
aacacaagtt caactgacca tatccttcca tgacctgaat agatgctatc ctttatcacg 420
atgttcaatt gcctttgaaa gagagtagtc caggtatatt cctgatcaaa atttggcatt 480
tttgatgata ctactctaca cagatcagac tcatgtgcag aatcgtgcct ggagagagag 540
gtttggttaa gacagagatt tctggaaaca ttcaaattgc aaatggaaac ttgaacccca 600
caatctaatg aggaatgtac tggaaaaata atctgaagag ttgacaaatt gtgtactaga 660
ttgaacacat ggaatgcaat gccaatgaga ctttctgcac taaaacttat cctcatatgt 720
acaacaatga tgtgtgtatt atataacagt gatgtgtaca tttctgacac cccatacata 780
atatacacag tttgtataaa tgcatacatt taaaaatata tatgtacaat acagctaaca 840
taaaactgta gtacgcctga aggatattac tagtgcctaa tattgagtat gagtcactgc 900
gtgttcgcat caacttggaa gtgcagtaat tgttataaaa ttaatcagtg cagccaacat 960
tatttatgaa tcacatcttt gaaactgtgc agtagcatat acatatatat ttttaaataa 1020
cattttttcac agttttccag agttactgtt gaaatctgca tcaccaaaaa aaaaaaaaag 1080
caagatttttt ttaacaatgt agacactctt cagacccagt aatctgcgtg tgatttccta 1140
tttgtagatt cccaagagac tttagcagtc accagcctta atgcatgtac aggatattat 1200
tgtgacttaa tttatctgca gtttttaatc catgtgaaat tgggaatttt taaccgaact 1260
tggattaacc atgcctgcct ttctaaggtt gcaaatgtta cattaaatga tttatgttgt 1320
aaaaaaaaaa aa                                                    1332
```

<210> 53
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (3)
<223> "Xaa" at position 3 can be any amino acid

<220>
<223> Description of Artificial Sequence: Ctyokine
     receptor exctracellular motif found in many
     species.

<400> 53
Trp Ser Xaa Trp Ser
  1   5

<210> 54
<211> 2744
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (138)..(2387)

<400> 54
ctcgtgccga attcggcacg agaccgcgtg ttcgcgcctg gtagagattt ctcgaagaca 60

ccagtgggcc cgtgtggaac caaacctgcg cgcgtggccg gccgtggga caacgaggcc 120

gcggagacga aggcgca atg gcg agg aag tta tct gta atc ttg atc ctg   170
                      Met Ala Arg Lys Leu Ser Val Ile Leu Ile Leu
                      1   5   10

acc ttt gcc ctc tct gtc aca aat ccc ctt cat gaa cta aaa gca gct   218
Thr Phe Ala Leu Ser Val Thr Asn Pro Leu His Glu Leu Lys Ala Ala
            15   20   25

gct ttc ccc cag acc act gag aaa att agt ccg aat tgg gaa tct ggc   266
Ala Phe Pro Gln Thr Thr Glu Lys Ile Ser Pro Asn Trp Glu Ser Gly
        30   35   40

att aat gtt gac ttg gca att tcc aca cgg caa tat cat cta caa cag   314
Ile Asn Val Asp Leu Ala Ile Ser Thr Arg Gln Tyr His Leu Gln Gln
    45   50   55

ctt ttc tac cgc tat gga gaa aat aat tct ttg tca gtt gaa ggg ttc   362
Leu Phe Tyr Arg Tyr Gly Glu Asn Asn Ser Leu Ser Val Glu Gly Phe
60   65   70   75

aga aaa tta ctt caa aat ata ggc ata gat aag att aaa aga atc cat   410
Arg Lys Leu Leu Gln Asn Ile Gly Ile Asp Lys Ile Lys Arg Ile His
                80   85   90

ata cac cat gac cac gac cat cac tca gac cac gag cat cac tca gac   458
Ile His His Asp His Asp His His Ser Asp His Glu His His Ser Asp
                95   100   105

cat gag cgt cac tca gac cat gag cat cac tca gac cac gag cat cac   506
His Glu Arg His Ser Asp His Glu His His Ser Asp His Glu His His
        110   115   120

tct gac cat aat cat gct gct tct ggt aaa aat aag cga aaa gct ctt   554
Ser Asp His Asn His Ala Ala Ser Gly Lys Asn Lys Arg Lys Ala Leu
        125   130   135

tgc cca gac cat gac tca gat agt tca ggt aaa gat cct aga aac agc   602
Cys Pro Asp His Asp Ser Asp Ser Ser Gly Lys Asp Pro Arg Asn Ser
140   145   150   155

cag ggg aaa gga gct cac cga cca gaa cat gcc agt ggt aga agg aat   650
Gln Gly Lys Gly Ala His Arg Pro Glu His Ala Ser Gly Arg Arg Asn

53

```
gtc aag gac agt gtt agt gct agt gaa gtg acc tca act gtg tac aac    698
Val Lys Asp Ser Val Ser Ala Ser Glu Val Thr Ser Thr Val Tyr Asn
            175             180             185

act gtc tct gaa gga act cac ttt cta gag aca ata gag act cca aga    746
Thr Val Ser Glu Gly Thr His Phe Leu Glu Thr Ile Glu Thr Pro Arg
            190             195             200

cct gga aaa ctc ttc ccc aaa gat gta agc agc tcc act cca ccc agt    794
Pro Gly Lys Leu Phe Pro Lys Asp Val Ser Ser Ser Thr Pro Pro Ser
            205             210             215

gtc aca tca aag agc cgg gtg agc cgg ctg gct ggt agg aaa aca aat    842
Val Thr Ser Lys Ser Arg Val Ser Arg Leu Ala Gly Arg Lys Thr Asn
220             225             230             235

gaa tct gtg agt gag ccc cga aaa ggc ttt atg tat tcc aga aac aca    890
Glu Ser Val Ser Glu Pro Arg Lys Gly Phe Met Tyr Ser Arg Asn Thr
            240             245             250

aat gaa aat cct cag gag tgt ttc aat gca tca aag cta ctg aca tct    938
Asn Glu Asn Pro Gln Glu Cys Phe Asn Ala Ser Lys Leu Leu Thr Ser
            255             260             265

cat ggc atg ggc atc cag gtt ccg ctg aat gca aca gag ttc aac tat    986
His Gly Met Gly Ile Gln Val Pro Leu Asn Ala Thr Glu Phe Asn Tyr
            270             275             280

ctc tgt cca gcc atc atc aac caa att gat gct aga tct tgt ctg att    1034
Leu Cys Pro Ala Ile Ile Asn Gln Ile Asp Ala Arg Ser Cys Leu Ile
            285             290             295

cat aca agt gaa aag aag gct gaa atc cct cca aag acc tat tca tta    1082
His Thr Ser Glu Lys Lys Ala Glu Ile Pro Pro Lys Thr Tyr Ser Leu
300             305             310             315

caa ata gcc tgg gtt ggt ggt ttt ata gcc att tcc atc atc agt ttc    1130
Gln Ile Ala Trp Val Gly Gly Phe Ile Ala Ile Ser Ile Ile Ser Phe
            320             325             330

ctg tct ctg ctg ggg gtt atc tta gtg cct ctc atg aat cgg gtg ttt    1178
Leu Ser Leu Leu Gly Val Ile Leu Val Pro Leu Met Asn Arg Val Phe
            335             340             345

ttc aaa ttt ctc ctg agt ttc ctt gtg gca ctg gcc gtt ggg act ttg    1226
Phe Lys Phe Leu Leu Ser Phe Leu Val Ala Leu Ala Val Gly Thr Leu
            350             355             360

agt ggt gat gct ttt tta cac ctt ctt cca cat tct cat gca agt cac    1274
```

```
Ser Gly Asp Ala Phe Leu His Leu Leu Pro His Ser His Ala Ser His
    365             370             375

cac cat agt cat agc cat gaa gaa cca gca atg gaa atg aaa aga gga    1322
His His Ser His Ser His Glu Glu Pro Ala Met Glu Met Lys Arg Gly
380             385             390             395

cca ctt ttc agt cat ctg tct tct caa aac ata gaa gaa agt gcc tat    1370
Pro Leu Phe Ser His Leu Ser Ser Gln Asn Ile Glu Glu Ser Ala Tyr
            400             405             410

ttt gat tcc acg tgg aag ggt cta aca gct cta gga ggc ctg tat ttc    1418
Phe Asp Ser Thr Trp Lys Gly Leu Thr Ala Leu Gly Gly Leu Tyr Phe
            415             420             425

atg ttt ctt gtt gaa cat gtc ctc aca ttg atc aaa caa ttt aaa gat    1466
Met Phe Leu Val Glu His Val Leu Thr Leu Ile Lys Gln Phe Lys Asp
        430             435             440

aag aag aaa aag aat cag aag aaa cct gaa aat gat gat gat gtg gag    1514
Lys Lys Lys Lys Asn Gln Lys Lys Pro Glu Asn Asp Asp Asp Val Glu
        445             450             455

att aag aag cag ttg tcc aag tat gaa tct caa ctt tca aca aat gag    1562
Ile Lys Lys Gln Leu Ser Lys Tyr Glu Ser Gln Leu Ser Thr Asn Glu
460             465             470             475

gag aaa gta gat aca gat gat cga act gaa ggc tat tta cga gca gac    1610
Glu Lys Val Asp Thr Asp Asp Arg Thr Glu Gly Tyr Leu Arg Ala Asp
            480             485             490

tca caa gag ccc tcc cac ttt gat tct cag cag cct gca gtc ttg gaa    1658
Ser Gln Glu Pro Ser His Phe Asp Ser Gln Gln Pro Ala Val Leu Glu
            495             500             505

gaa gaa gag gtc atg ata gct cat gct cat cca cag gaa gtc tac aat    1706
Glu Glu Glu Val Met Ile Ala His Ala His Pro Gln Glu Val Tyr Asn
        510             515             520

gaa tat gta ccc aga ggg tgc aag aat aaa tgc cat tca cat ttc cac    1754
Glu Tyr Val Pro Arg Gly Cys Lys Asn Lys Cys His Ser His Phe His
    525             530             535

gat aca ctc ggc cag tca gac gat ctc att cac cac cat cat gac tac    1802
Asp Thr Leu Gly Gln Ser Asp Asp Leu Ile His His His His Asp Tyr
540             545             550             555

cat cat att ctc cat cat cac cac cac caa aac cac cat cct cac agt    1850
His His Ile Leu His His His His His Gln Asn His His Pro His Ser
            560             565             570
```

55

```
cac agc cag cgc tac tct cgg gag gag ctg aaa gat gcc ggc gtc gcc    1898
His Ser Gln Arg Tyr Ser Arg Glu Glu Leu Lys Asp Ala Gly Val Ala
            575                 580                 585

act ttg gcc tgg atg gtg ata atg ggt gat ggc ctg cac aat ttc agc    1946
Thr Leu Ala Trp Met Val Ile Met Gly Asp Gly Leu His Asn Phe Ser
            590                 595                 600

gat ggc cta gca att ggt gct gct ttt act gaa ggc tta tca agt ggt    1994
Asp Gly Leu Ala Ile Gly Ala Ala Phe Thr Glu Gly Leu Ser Ser Gly
            605                 610                 615

tta agt act tct gtt gct gtg ttc tgt cat gag ttg cct cat gaa tta    2042
Leu Ser Thr Ser Val Ala Val Phe Cys His Glu Leu Pro His Glu Leu
620                 625                 630                 635

ggt gac ttt gct gtt cta cta aag gct ggc atg acc gtt aag cag gct    2090
Gly Asp Phe Ala Val Leu Leu Lys Ala Gly Met Thr Val Lys Gln Ala
            640                 645                 650

gtc ctt tat aat gca ttg tca gcc atg ctg gcg tat ctt gga atg gca    2138
Val Leu Tyr Asn Ala Leu Ser Ala Met Leu Ala Tyr Leu Gly Met Ala
            655                 660                 665

aca gga att ttc att ggt cat tat gct gaa aat gtt tct atg tgg ata    2186
Thr Gly Ile Phe Ile Gly His Tyr Ala Glu Asn Val Ser Met Trp Ile
            670                 675                 680

ttt gca ctt act gct ggc tta ttc atg tat gtt gct ctg gtt gat atg    2234
Phe Ala Leu Thr Ala Gly Leu Phe Met Tyr Val Ala Leu Val Asp Met
            685                 690                 695

gta cct gaa atg ctg cac aat gat gct agt gac cat gga tgt agc cgc    2282
Val Pro Glu Met Leu His Asn Asp Ala Ser Asp His Gly Cys Ser Arg
700                 705                 710                 715

tgg ggg tat ttc ttt tta cag aat gct ggg atg ctt ttg ggt ttt gga    2330
Trp Gly Tyr Phe Phe Leu Gln Asn Ala Gly Met Leu Leu Gly Phe Gly
            720                 725                 730

att atg tta ctt att tcc ata ttt gaa cat aaa atc gtg ttt cgt ata    2378
Ile Met Leu Leu Ile Ser Ile Phe Glu His Lys Ile Val Phe Arg Ile
            735                 740                 745

aat ttc tag ttaaggttta aatgctagag tagcttaaaa agttgtcata    2427
Asn Phe


gtttcagtag gtcataggga gatgagtttg tatgctgtac tatgcagcgt ttaaagttag 2487

tgggttttgt gatttttgta ttgaatattg ctgtctgtta caaagtcagt taaaggtacg 2547
```

56

```
ttttaatatt taagttattc tatcttggag ataaaatctg tatgtgcaat tcaccggtat 2607

taccagttta ttatgtaaac aagagatttg gcatgacatg ttctgtatgt ttcagggaaa 2667

aatgtcttta atgctttttc aagaactaac acagttattc ctatactgga ttttaggtct 2727

ctgaagaact gctggtg                                                  2744
```

<210> 55
<211> 749
<212> PRT
<213> Homo sapiens

<400> 55

```
Met Ala Arg Lys Leu Ser Val Ile Leu Ile Leu Thr Phe Ala Leu Ser
 1               5                  10                  15
Val Thr Asn Pro Leu His Glu Leu Lys Ala Ala Ala Phe Pro Gln Thr
                20                  25                  30
Thr Glu Lys Ile Ser Pro Asn Trp Glu Ser Gly Ile Asn Val Asp Leu
            35                  40                  45
Ala Ile Ser Thr Arg Gln Tyr His Leu Gln Gln Leu Phe Tyr Arg Tyr
        50                  55                  60
Gly Glu Asn Asn Ser Leu Ser Val Glu Gly Phe Arg Lys Leu Leu Gln
65                  70                  75                  80
Asn Ile Gly Ile Asp Lys Ile Lys Arg Ile His Ile His His Asp His
                85                  90                  95
Asp His His Ser Asp His Glu His His Ser Asp His Glu Arg His Ser
            100                 105                 110
Asp His Glu His His Ser Asp His Glu His His Ser Asp His Asn His
        115                 120                 125
Ala Ala Ser Gly Lys Asn Lys Arg Lys Ala Leu Cys Pro Asp His Asp
    130                 135                 140
Ser Asp Ser Ser Gly Lys Asp Pro Arg Asn Ser Gln Gly Lys Gly Ala
145                 150                 155                 160
His Arg Pro Glu His Ala Ser Gly Arg Arg Asn Val Lys Asp Ser Val
                165                 170                 175
Ser Ala Ser Glu Val Thr Ser Thr Val Tyr Asn Thr Val Ser Glu Gly
            180                 185                 190
Thr His Phe Leu Glu Thr Ile Glu Thr Pro Arg Pro Gly Lys Leu Phe
        195                 200                 205
Pro Lys Asp Val Ser Ser Ser Thr Pro Pro Ser Val Thr Ser Lys Ser
    210                 215                 220
Arg Val Ser Arg Leu Ala Gly Arg Lys Thr Asn Glu Ser Val Ser Glu
225                 230                 235                 240
Pro Arg Lys Gly Phe Met Tyr Ser Arg Asn Thr Asn Glu Asn Pro Gln
                245                 250                 255
Glu Cys Phe Asn Ala Ser Lys Leu Leu Thr Ser His Gly Met Gly Ile
            260                 265                 270
Gln Val Pro Leu Asn Ala Thr Glu Phe Asn Tyr Leu Cys Pro Ala Ile
        275                 280                 285
```

57

```
Ile Asn Gln Ile Asp Ala Arg Ser Cys Leu Ile His Thr Ser Glu Lys
    290                 295                 300
Lys Ala Glu Ile Pro Pro Lys Thr Tyr Ser Leu Gln Ile Ala Trp Val
305                 310                 315                 320
Gly Gly Phe Ile Ala Ile Ser Ile Ile Ser Phe Leu Ser Leu Leu Gly
                325                 330                 335
Val Ile Leu Val Pro Leu Met Asn Arg Val Phe Phe Lys Phe Leu Leu
                340                 345                 350
Ser Phe Leu Val Ala Leu Ala Val Gly Thr Leu Ser Gly Asp Ala Phe
                355                 360                 365
Leu His Leu Leu Pro His Ser His Ala Ser His His His Ser His Ser
    370                 375                 380
His Glu Glu Pro Ala Met Glu Met Lys Arg Gly Pro Leu Phe Ser His
385                 390                 395                 400
Leu Ser Ser Gln Asn Ile Glu Glu Ser Ala Tyr Phe Asp Ser Thr Trp
                405                 410                 415
Lys Gly Leu Thr Ala Leu Gly Gly Leu Tyr Phe Met Phe Leu Val Glu
                420                 425                 430
His Val Leu Thr Leu Ile Lys Gln Phe Lys Asp Lys Lys Lys Lys Asn
    435                 440                 445
Gln Lys Lys Pro Glu Asn Asp Asp Asp Val Glu Ile Lys Lys Gln Leu
    450                 455                 460
Ser Lys Tyr Glu Ser Gln Leu Ser Thr Asn Glu Glu Lys Val Asp Thr
465                 470                 475                 480
Asp Asp Arg Thr Glu Gly Tyr Leu Arg Ala Asp Ser Gln Glu Pro Ser
                485                 490                 495
His Phe Asp Ser Gln Gln Pro Ala Val Leu Glu Glu Glu Glu Val Met
                500                 505                 510
Ile Ala His Ala His Pro Gln Glu Val Tyr Asn Glu Tyr Val Pro Arg
    515                 520                 525
Gly Cys Lys Asn Lys Cys His Ser His Phe His Asp Thr Leu Gly Gln
    530                 535                 540
Ser Asp Asp Leu Ile His His His His Asp Tyr His His Ile Leu His
545                 550                 555                 560
His His His His Gln Asn His His Pro His Ser His Ser Gln Arg Tyr
                565                 570                 575
Ser Arg Glu Glu Leu Lys Asp Ala Gly Val Ala Thr Leu Ala Trp Met
                580                 585                 590
Val Ile Met Gly Asp Gly Leu His Asn Phe Ser Asp Gly Leu Ala Ile
    595                 600                 605
Gly Ala Ala Phe Thr Glu Gly Leu Ser Ser Gly Leu Ser Thr Ser Val
    610                 615                 620
Ala Val Phe Cys His Glu Leu Pro His Glu Leu Gly Asp Phe Ala Val
625                 630                 635                 640
Leu Leu Lys Ala Gly Met Thr Val Lys Gln Ala Val Leu Tyr Asn Ala
                645                 650                 655
Leu Ser Ala Met Leu Ala Tyr Leu Gly Met Ala Thr Gly Ile Phe Ile
                660                 665                 670
Gly His Tyr Ala Glu Asn Val Ser Met Trp Ile Phe Ala Leu Thr Ala
    675                 680                 685
Gly Leu Phe Met Tyr Val Ala Leu Val Asp Met Val Pro Glu Met Leu
```

58

```
              690                        695                    700
His Asn Asp Ala Ser Asp His Gly Cys Ser Arg Trp Gly Tyr Phe Phe
705                        710                    715                    720
Leu Gln Asn Ala Gly Met Leu Leu Gly Phe Gly Ile Met Leu Leu Ile
                    725                    730                    735
Ser Ile Phe Glu His Lys Ile Val Phe Arg Ile Asn Phe
                    740                    745
```

```
<210> 56
<211> 293
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (190)
<223> "n" at position 190 can be any base

<400> 56
ttttttttac tgtgaaattc taaaatcata tttattcacc aattcacaga aagtgtcata 60
acgaccacca acatgaatca gtttgtaggc atttacaagc cacagctgaa aataaaaatc 120
tgtctgtgtt gaataggcat ttaacaaatt acttgaaaac tgcaagaatc ataattatta 180
taaatttaan gtttgtgatt caaacatggg taagatcaca gtcatgggga gaagcccaac 240
agattcctgt gatgatcctt attttcttcc tatatcttta tatacatagg agg 293
```

```
<210> 57
<211> 2053
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (85)..(1347)

<400> 57
ccggctcgcg ccctccgggc ccagcctccc gagccttcgg agcgggcgcc gtcccagccc 60

agctccgggg aaacgcgagc cgcg atg cct ggg ggg tgc tcc cgg ggc ccc      111
                           Met Pro Gly Gly Cys Ser Arg Gly Pro
                            1               5

gcc gcc ggg gac ggg cgt ctg cgg ctg gcg cga cta gcg ctg gta ctc   159
Ala Ala Gly Asp Gly Arg Leu Arg Leu Ala Arg Leu Ala Leu Val Leu
 10               15                20                    25

ctg ggc tgg gtc tcc tcg tct tct ccc acc tcc tcg gca tcc tcc ttc   207
Leu Gly Trp Val Ser Ser Ser Ser Pro Thr Ser Ser Ala Ser Ser Phe
                30                    35                    40
```

59

```
tcc tcc tcg gcg ccg ttc ctg gct tcc gcc gtg tcc gcc cag ccc ccg    255
Ser Ser Ser Ala Pro Phe Leu Ala Ser Ala Val Ser Ala Gln Pro Pro
            45              50                  55

ctg ccg gac cag tgc ccc gcg ctg tgc gag tgc tcc gag gca gcg cgc    303
Leu Pro Asp Gln Cys Pro Ala Leu Cys Glu Cys Ser Glu Ala Ala Arg
            60              65                  70

aca gtc aag tgc gtt aac cgc aat ctg acc gag gtg ccc acg gac ctg    351
Thr Val Lys Cys Val Asn Arg Asn Leu Thr Glu Val Pro Thr Asp Leu
        75              80                  85

ccc gcc tac gtg cgc aac ctc ttc ctt acc ggc aac cag ctg gcc gtg    399
Pro Ala Tyr Val Arg Asn Leu Phe Leu Thr Gly Asn Gln Leu Ala Val
90                  95                  100                 105

ctc cct gcc ggc gcc ttc gcc cgc cgg ccg ccg ctg gcg gag ctg gcc    447
Leu Pro Ala Gly Ala Phe Ala Arg Arg Pro Pro Leu Ala Glu Leu Ala
                110                 115                 120

gcg ctc aac ctc agc ggc agc cgc ctg gac gag gtg cgc gcg ggc gcc    495
Ala Leu Asn Leu Ser Gly Ser Arg Leu Asp Glu Val Arg Ala Gly Ala
                125                 130                 135

ttc gag cat ctg ccc agc ctg cgc cag ctc gac ctc agc cac aac cca    543
Phe Glu His Leu Pro Ser Leu Arg Gln Leu Asp Leu Ser His Asn Pro
            140                 145                 150

ctg gcc gac ctc agt ccc ttc gct ttc tcg ggc agc aat gcc agc gtc    591
Leu Ala Asp Leu Ser Pro Phe Ala Phe Ser Gly Ser Asn Ala Ser Val
        155                 160                 165

tcg gcc ccc agt ccc ctt gtg gaa ctg atc ctg aac cac atc gtg ccc    639
Ser Ala Pro Ser Pro Leu Val Glu Leu Ile Leu Asn His Ile Val Pro
170                 175                 180                 185

cct gaa gat gag cgg cag aac cgg agc ttc gag ggc atg gtg gtg gcg    687
Pro Glu Asp Glu Arg Gln Asn Arg Ser Phe Glu Gly Met Val Val Ala
                190                 195                 200

gcc ctg ctg gcg ggc cgt gca ctg cag ggg ctc cgc cgc ttg gag ctg    735
Ala Leu Leu Ala Gly Arg Ala Leu Gln Gly Leu Arg Arg Leu Glu Leu
                205                 210                 215

gcc agc aac cac ttc ctt tac ctg ccg cgg gat gtg ctg gcc caa ctg    783
Ala Ser Asn His Phe Leu Tyr Leu Pro Arg Asp Val Leu Ala Gln Leu
                220                 225                 230

ccc agc ctc agg cac ctg gac tta agt aat aat tcg ctg gtg agc ctg    831
Pro Ser Leu Arg His Leu Asp Leu Ser Asn Asn Ser Leu Val Ser Leu
        235                 240                 245
```

60

```
acc tac gtg tcc ttc cgc aac ctg aca cat cta gaa agc ctc cac ctg   879
Thr Tyr Val Ser Phe Arg Asn Leu Thr His Leu Glu Ser Leu His Leu
250             255             260             265

gag gac aat gcc ctc aag gtc ctt cac aat ggc acc ctg gct gag ttg   927
Glu Asp Asn Ala Leu Lys Val Leu His Asn Gly Thr Leu Ala Glu Leu
                270             275             280

caa ggt cta ccc cac att agg gtt ttc ctg gac aac aat ccc tgg gtc   975
Gln Gly Leu Pro His Ile Arg Val Phe Leu Asp Asn Asn Pro Trp Val
                285             290             295

tgc gac tgc cac atg gca gac atg gtg acc tgg ctc aag gaa aca gag   1023
Cys Asp Cys His Met Ala Asp Met Val Thr Trp Leu Lys Glu Thr Glu
            300             305             310

gta gtg cag ggc aaa gac cgg ctc acc tgt gca tat ccg gaa aaa atg   1071
Val Val Gln Gly Lys Asp Arg Leu Thr Cys Ala Tyr Pro Glu Lys Met
        315             320             325

agg aat cgg gtc ctc ttg gaa ctc aac agt gct gac ctg gac tgt gac   1119
Arg Asn Arg Val Leu Leu Glu Leu Asn Ser Ala Asp Leu Asp Cys Asp
330             335             340             345

ccg att ctt ccc cca tcc ctg caa acc tct tat gtc ttc ctg ggt att   1167
Pro Ile Leu Pro Pro Ser Leu Gln Thr Ser Tyr Val Phe Leu Gly Ile
                350             355             360

gtt tta gcc ctg ata ggc gct att ttc ctc ctg gtt ttg tat ttg aac   1215
Val Leu Ala Leu Ile Gly Ala Ile Phe Leu Leu Val Leu Tyr Leu Asn
                365             370             375

cgc aag ggg ata aaa aag tgg atg cat aac atc aga gat gcc tgc agg   1263
Arg Lys Gly Ile Lys Lys Trp Met His Asn Ile Arg Asp Ala Cys Arg
        380             385             390

gat cac atg gaa ggg tat cat tac aga tat gaa atc aat gcg gac ccc   1311
Asp His Met Glu Gly Tyr His Tyr Arg Tyr Glu Ile Asn Ala Asp Pro
        395             400             405

aga tta aca aac ctc agt tct aac tcg gat gtc tga gaaatattag         1357
Arg Leu Thr Asn Leu Ser Ser Asn Ser Asp Val
410             415             420

aggacagacc aaggacaact ctgcatgaga tgtagactta agctttatcc ctactaggct 1417

tgctccactt tcatcctcca ctatagatac aacggacttt gactaaaagc agtgaagggg 1477

atttgcttcc ttgttatgta aagtttctcg gtgtgttctg ttaatgtaag acgatgaaca 1537

gttgtgtata gtgttttacc ctcttctttt tcttggaact cctcaacacg tatggaggga 1597
```

61

```
tttttcaggt ttcagcatga acatgggctt cttgctgtct gtctctctct cagtacagtt 1657

caaggtgtag caagtgtacc cacacagata gcattcaaca aaagctgcct caactttttc 1717

gagaaaaata ctttattcat aaatatcagt tttattctca tgtacctaag ttgtggagaa 1777

aataattgca tcctataaac tgcctgcaga cgttagcagg ctcttcaaaa taactccatg 1837

gtgcacagga gcacctgcat ccaagagcat gcttacattt tactgttctg catattacaa 1897

aaaataactt gcaacttcat aacttctttg acaaagtaaa ttactttttt gattgcagtt 1957

tatatgaaaa tgtactgatt ttttttttaat aaactgcatc gagatccaac cgactgaatt 2017

gttaaaaaaa aaaaaaaata aagattctta aaagaa                              2053
```

<210> 58
<211> 420
<212> PRT
<213> Homo sapiens

<400> 58
```
Met Pro Gly Gly Cys Ser Arg Gly Pro Ala Ala Gly Asp Gly Arg Leu
 1               5                  10                  15
Arg Leu Ala Arg Leu Ala Leu Val Leu Leu Gly Trp Val Ser Ser Ser
            20                  25                  30
Ser Pro Thr Ser Ser Ala Ser Ser Phe Ser Ser Ser Ala Pro Phe Leu
            35                  40                  45
Ala Ser Ala Val Ser Ala Gln Pro Pro Leu Pro Asp Gln Cys Pro Ala
        50                  55                  60
Leu Cys Glu Cys Ser Glu Ala Ala Arg Thr Val Lys Cys Val Asn Arg
65                  70                  75                  80
Asn Leu Thr Glu Val Pro Thr Asp Leu Pro Ala Tyr Val Arg Asn Leu
                85                  90                  95
Phe Leu Thr Gly Asn Gln Leu Ala Val Leu Pro Ala Gly Ala Phe Ala
            100                 105                 110
Arg Arg Pro Pro Leu Ala Glu Leu Ala Ala Leu Asn Leu Ser Gly Ser
            115                 120                 125
Arg Leu Asp Glu Val Arg Ala Gly Ala Phe Glu His Leu Pro Ser Leu
        130                 135                 140
Arg Gln Leu Asp Leu Ser His Asn Pro Leu Ala Asp Leu Ser Pro Phe
145                 150                 155                 160
Ala Phe Ser Gly Ser Asn Ala Ser Val Ser Ala Pro Ser Pro Leu Val
                165                 170                 175
Glu Leu Ile Leu Asn His Ile Val Pro Pro Glu Asp Glu Arg Gln Asn
                180                 185                 190
Arg Ser Phe Glu Gly Met Val Val Ala Ala Leu Leu Ala Gly Arg Ala
            195                 200                 205
Leu Gln Gly Leu Arg Arg Leu Glu Leu Ala Ser Asn His Phe Leu Tyr
        210                 215                 220
```

62

```
Leu Pro Arg Asp Val Leu Ala Gln Leu Pro Ser Leu Arg His Leu Asp
225                 230                 235                 240
Leu Ser Asn Asn Ser Leu Val Ser Leu Thr Tyr Val Ser Phe Arg Asn
                245                 250                 255
Leu Thr His Leu Glu Ser Leu His Leu Glu Asp Asn Ala Leu Lys Val
                260                 265                 270
Leu His Asn Gly Thr Leu Ala Glu Leu Gln Gly Leu Pro His Ile Arg
            275                 280                 285
Val Phe Leu Asp Asn Asn Pro Trp Val Cys Asp Cys His Met Ala Asp
        290                 295                 300
Met Val Thr Trp Leu Lys Glu Thr Glu Val Val Gln Gly Lys Asp Arg
305                 310                 315                 320
Leu Thr Cys Ala Tyr Pro Glu Lys Met Arg Asn Arg Val Leu Leu Glu
                325                 330                 335
Leu Asn Ser Ala Asp Leu Asp Cys Asp Pro Ile Leu Pro Pro Ser Leu
                340                 345                 350
Gln Thr Ser Tyr Val Phe Leu Gly Ile Val Leu Ala Leu Ile Gly Ala
            355                 360                 365
Ile Phe Leu Leu Val Leu Tyr Leu Asn Arg Lys Gly Ile Lys Lys Trp
        370                 375                 380
Met His Asn Ile Arg Asp Ala Cys Arg Asp His Met Glu Gly Tyr His
385                 390                 395                 400
Tyr Arg Tyr Glu Ile Asn Ala Asp Pro Arg Leu Thr Asn Leu Ser Ser
                405                 410                 415
Asn Ser Asp Val
            420




<210> 59
<211> 232
<212> DNA
<213> Homo sapiens

<400> 59
tttttaatta tactcttta ttgaaagaaa aaacaataca atggacttta aaaagctaca   60
tttgttatgg ttcataagga cagaggttta cacaggtttt atatatgtac acactgacaa  120
tactatatca caacatcaga ggcaccattt ttgccacaga attaggtaat gaataaaact  180
tctccaaatt aatctgttta aaaaatatct aaaatggtac agtatatttg ag          232


<210> 60
<211> 281
<212> DNA
<213> Homo sapiens

<400> 60
taccaaaata tctgtattat ctataaaaat tgaactctaa tgagtcactg atacgggagg   60
cagcaatacc cgactgtgct gacatgcaga aggaagacag ctctgtccca ccaaccctat  120
agcagaacat ttgtattgag tggcacgtgg gctgagtcat ttgtaaggtc tcaaaaacct  180
ggacactttg gaacgtagca atcggatgaa cgatcttgga aacatctctc gggactcctg  240
```

ggctgtgtac ttgaaatagt tctggggatg ggccaggaca t   281

<210> 61
<211> 3085
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (256)..(3012)

<400> 61
gagcagccaa aaggcccgcg gagtcgcgct gggccgcccc ggcgcagctg aaccggggggc 60

cgcgcctgcc aggccgacgg gtctggccca gcctggcgcc aaggggttcg tgcgctgtgg 120

agacgcggag ggtcgaggcg gcgcggcctg agtgaaaccc aatggaaaaa gcatgacatt 180

tagaagtaga agacttagct tcaaatccct actccttcac ttactaattt tgtgatttgg 240

aaatatccgc gcaag atg ttg acg ttg cag act tgg gta gtg caa gcc ttg   291
               Met Leu Thr Leu Gln Thr Trp Val Val Gln Ala Leu
                1   5   10

ttt att ttc ctc acc act gaa tct aca ggt gaa ctt cta gat cca tgt   339
Phe Ile Phe Leu Thr Thr Glu Ser Thr Gly Glu Leu Leu Asp Pro Cys
            15   20   25

ggt tat atc agt cct gaa tct cca gtt gta caa ctt cat tct aat ttc   387
Gly Tyr Ile Ser Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe
    30   35   40

act gca gtt tgt gtg cta aag gaa aaa tgt atg gat tat ttt cat gta   435
Thr Ala Val Cys Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val
45   50   55   60

aat gct aat tac att gtc tgg aaa aca aac cat ttt act att cct aag   483
Asn Ala Asn Tyr Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys
                65   70   75

gag caa tat act atc ata aac aga aca gca tcc agt gtc acc ttt aca   531
Glu Gln Tyr Thr Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr
                80   85   90

gat ata gct tca tta aat att cag ctc act tgc aac att ctt aca ttc   579
Asp Ile Ala Ser Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe
            95   100   105

gga cag ctt gaa cag aat gtt tat gga atc aca ata att tca ggc ttg   627
Gly Gln Leu Glu Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu

64

```
cct cca gaa aaa cct aaa aat ttg agt tgc att gtg aac gag ggg aag   675
Pro Pro Glu Lys Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys
125             130             135             140

aaa atg agg tgt gag tgg gat ggt gga agg gaa aca cac ttg gag aca   723
Lys Met Arg Cys Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr
            145             150             155

aac ttc act tta aaa tct gaa tgg gca aca cac aag ttt gct gat tgc   771
Asn Phe Thr Leu Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys
                160             165             170

aaa gca aaa cgt gac acc ccc acc tca tgc act gtt gat tat tct act   819
Lys Ala Lys Arg Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr
                175             180             185

gtg tat ttt gtc aac att gaa gtc tgg gta gaa gca gag aat gcc ctt   867
Val Tyr Phe Val Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu
            190             195             200

ggg aag gtt aca tca gat cat atc aat ttt gat cct gta tat aaa gtg   915
Gly Lys Val Thr Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val
205             210             215             220

aag ccc aat ccg cca cat aat tta tca gtg atc aac tca gag gaa ctg   963
Lys Pro Asn Pro Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu
                225             230             235

tct agt atc tta aaa ttg aca tgg acc aac cca agt att aag agt gtt  1011
Ser Ser Ile Leu Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val
                240             245             250

ata ata cta aaa tat aac att caa tat agg acc aaa gat gcc tca act  1059
Ile Ile Leu Lys Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr
                255             260             265

tgg agc cag att cct cct gaa gac aca gca tcc acc cga tct tca ttc  1107
Trp Ser Gln Ile Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe
            270             275             280

act gtc caa gac ctt aaa cct ttt aca gaa tat gtg ttt agg att cgc  1155
Thr Val Gln Asp Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg
285             290             295             300

tgt atg aag gaa gat ggt aag gga tac tgg agt gac tgg agt gaa gaa  1203
Cys Met Lys Glu Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu
            305             310             315

gca agt ggg atc acc tat gaa gat aga cca tct aaa gca cca agt ttc  1251
```

```
Ala Ser Gly Ile Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe
            320             325             330

tgg tat aaa ata gat cca tcc cat act caa ggc tac aga act gta caa    1299
Trp Tyr Lys Ile Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln
            335             340             345

ctc gtg tgg aag aca ttg cct cct ttt gaa gcc aat gga aaa atc ttg    1347
Leu Val Trp Lys Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu
            350             355             360

gat tat gaa gtg act ctc aca aga tgg aaa tca cat tta caa aat tac    1395
Asp Tyr Glu Val Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr
365             370             375             380

aca gtt aat gcc aca aaa ctg aca gta aat ctc aca aat gat cgc tat    1443
Thr Val Asn Ala Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr
            385             390             395

cta gca acc cta aca gta aga aat ctt gtt ggc aaa tca gat gca gct    1491
Leu Ala Thr Leu Thr Val Arg Asn Leu Val Gly Lys Ser Asp Ala Ala
            400             405             410

gtt tta act atc cct gcc tgt gac ttt caa gct act cac cct gta atg    1539
Val Leu Thr Ile Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met
            415             420             425

gat ctt aaa gca ttc ccc aaa gat aac atg ctt tgg gtg gaa tgg act    1587
Asp Leu Lys Ala Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr
            430             435             440

act cca agg gaa tct gta aag aaa tat ata ctt gag tgg tgt gtg tta    1635
Thr Pro Arg Glu Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu
445             450             455             460

tca gat aaa gca ccc tgt atc aca gac tgg caa caa gaa gat ggt acc    1683
Ser Asp Lys Ala Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr
                465             470             475

gtg cat cgc acc tat tta aga ggg aac tta gca gag agc aaa tgc tat    1731
Val His Arg Thr Tyr Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr
                480             485             490

ttg ata aca gtt act cca gta tat gct gat gga cca gga agc cct gaa    1779
Leu Ile Thr Val Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu
            495             500             505

tcc ata aag gca tac ctt aaa caa gct cca cct tcc aaa gga cct act    1827
Ser Ile Lys Ala Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr
510             515             520
```

```
gtt cgg aca aaa aaa gta ggg aaa aac gaa gct gtc tta gag tgg gac        1875
Val Arg Thr Lys Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp
525             530             535             540

caa ctt cct gtt gat gtt cag aat gga ttt atc aga aat tat act ata        1923
Gln Leu Pro Val Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile
            545             550             555

ttt tat aga acc atc att gga aat gaa act gct gtg aat gtg gat tct        1971
Phe Tyr Arg Thr Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser
        560             565             570

tcc cac aca gaa tat aca ttg tcc tct ttg act agt gac aca ttg tac        2019
Ser His Thr Glu Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr
        575             580             585

atg gta cga atg gca gca tac aca gat gaa ggt ggg aag gat ggt cca        2067
Met Val Arg Met Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro
        590             595             600

gaa ttc act ttt act acc cca aag ttt gct caa gga gaa att gaa gcc        2115
Glu Phe Thr Phe Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ala
605             610             615             620

ata gtc gtg cct gtt tgc tta gca ttc cta ttg aca act ctt ctg gga        2163
Ile Val Val Pro Val Cys Leu Ala Phe Leu Leu Thr Thr Leu Leu Gly
            625             630             635

gtg ctg ttc tgc ttt aat aag cga gac cta att aaa aaa cac atc tgg        2211
Val Leu Phe Cys Phe Asn Lys Arg Asp Leu Ile Lys Lys His Ile Trp
            640             645             650

cct aat gtt cca gat cct tca aag agt cat att gcc cag tgg tca cct        2259
Pro Asn Val Pro Asp Pro Ser Lys Ser His Ile Ala Gln Trp Ser Pro
            655             660             665

cac act cct cca agg cac aat ttt aat tca aaa gat caa atg tat tca        2307
His Thr Pro Pro Arg His Asn Phe Asn Ser Lys Asp Gln Met Tyr Ser
        670             675             680

gat ggc aat ttc act gat gta agt gtt gtg gaa ata gaa gca aat gac        2355
Asp Gly Asn Phe Thr Asp Val Ser Val Val Glu Ile Glu Ala Asn Asp
685             690             695             700

aaa aag cct ttt cca gaa gat ctg aaa tca ttg gac ctg ttc aaa aag        2403
Lys Lys Pro Phe Pro Glu Asp Leu Lys Ser Leu Asp Leu Phe Lys Lys
            705             710             715

gaa aaa att aat act gaa gga cac agc agt ggt att ggg ggg tct tca        2451
Glu Lys Ile Asn Thr Glu Gly His Ser Ser Gly Ile Gly Gly Ser Ser
            720             725             730
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67

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tgc atg tca tct tct agg cca agc att tct agc agt gat gaa aat gaa   2499
Cys Met Ser Ser Ser Arg Pro Ser Ile Ser Ser Ser Asp Glu Asn Glu
        735                 740                 745


tct tca caa aac act tcg agc act gtc cag tat tct acc gtg gta cac   2547
Ser Ser Gln Asn Thr Ser Ser Thr Val Gln Tyr Ser Thr Val Val His
        750                 755                 760


agt ggc tac aga cac caa gtt ccg tca gtc caa gtc ttc tca aga tcc   2595
Ser Gly Tyr Arg His Gln Val Pro Ser Val Gln Val Phe Ser Arg Ser
765                 770                 775                 780


gag tct acc cag ccc ttg tta gat tca gag gag cgg cca gaa gat cta   2643
Glu Ser Thr Gln Pro Leu Leu Asp Ser Glu Glu Arg Pro Glu Asp Leu
                785                 790                 795


caa tta gta gat cat gta gat ggc ggt gat ggt att ttg ccc agg caa   2691
Gln Leu Val Asp His Val Asp Gly Gly Asp Gly Ile Leu Pro Arg Gln
                800                 805                 810


cag tac ttc aaa cag aac tgc agt cag cat gaa tcc agt cca gat att   2739
Gln Tyr Phe Lys Gln Asn Cys Ser Gln His Glu Ser Ser Pro Asp Ile
        815                 820                 825


tca cat ttt gaa agg tca aag caa gtt tca tca gtc aat gag gaa gat   2787
Ser His Phe Glu Arg Ser Lys Gln Val Ser Ser Val Asn Glu Glu Asp
        830                 835                 840


ttt gtt aga ctt aaa cag cag att tca gat cat att tca caa tcc tgt   2835
Phe Val Arg Leu Lys Gln Gln Ile Ser Asp His Ile Ser Gln Ser Cys
845                 850                 855                 860


gga tct ggg caa atg aaa atg ttt cag gaa gtt tct gca gca gat gct   2883
Gly Ser Gly Gln Met Lys Met Phe Gln Glu Val Ser Ala Ala Asp Ala
                865                 870                 875


ttt ggt cca ggt act gag gga caa gta gaa aga ttt gaa aca gtt ggc   2931
Phe Gly Pro Gly Thr Glu Gly Gln Val Glu Arg Phe Glu Thr Val Gly
                880                 885                 890


atg gag gct gcg act gat gaa ggc atg cct aaa agt tac tta cca cag   2979
Met Glu Ala Ala Thr Asp Glu Gly Met Pro Lys Ser Tyr Leu Pro Gln
                895                 900                 905


act gta cgg caa ggc ggc tac atg cct cag tga aggactagta gttcctgcta 3032
Thr Val Arg Gln Gly Gly Tyr Met Pro Gln
        910                 915


caacttcagc agtacctata aagtaaagct aaaatgattt tatctgtgaa ttc        3085
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68

<210> 62
<211> 918
<212> PRT
<213> Homo sapiens

<400> 62

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Met Leu Thr Leu Gln Thr Trp Val Val Gln Ala Leu Phe Ile Phe Leu
 1               5                  10                  15
Thr Thr Glu Ser Thr Gly Glu Leu Leu Asp Pro Cys Gly Tyr Ile Ser
            20                  25                  30
Pro Glu Ser Pro Val Val Gln Leu His Ser Asn Phe Thr Ala Val Cys
        35                  40                  45
Val Leu Lys Glu Lys Cys Met Asp Tyr Phe His Val Asn Ala Asn Tyr
    50                  55                  60
Ile Val Trp Lys Thr Asn His Phe Thr Ile Pro Lys Glu Gln Tyr Thr
65                  70                  75                  80
Ile Ile Asn Arg Thr Ala Ser Ser Val Thr Phe Thr Asp Ile Ala Ser
                85                  90                  95
Leu Asn Ile Gln Leu Thr Cys Asn Ile Leu Thr Phe Gly Gln Leu Glu
            100                 105                 110
Gln Asn Val Tyr Gly Ile Thr Ile Ile Ser Gly Leu Pro Pro Glu Lys
        115                 120                 125
Pro Lys Asn Leu Ser Cys Ile Val Asn Glu Gly Lys Lys Met Arg Cys
    130                 135                 140
Glu Trp Asp Gly Gly Arg Glu Thr His Leu Glu Thr Asn Phe Thr Leu
145                 150                 155                 160
Lys Ser Glu Trp Ala Thr His Lys Phe Ala Asp Cys Lys Ala Lys Arg
                165                 170                 175
Asp Thr Pro Thr Ser Cys Thr Val Asp Tyr Ser Thr Val Tyr Phe Val
            180                 185                 190
Asn Ile Glu Val Trp Val Glu Ala Glu Asn Ala Leu Gly Lys Val Thr
            195                 200                 205
Ser Asp His Ile Asn Phe Asp Pro Val Tyr Lys Val Lys Pro Asn Pro
    210                 215                 220
Pro His Asn Leu Ser Val Ile Asn Ser Glu Glu Leu Ser Ser Ile Leu
225                 230                 235                 240
Lys Leu Thr Trp Thr Asn Pro Ser Ile Lys Ser Val Ile Ile Leu Lys
                245                 250                 255
Tyr Asn Ile Gln Tyr Arg Thr Lys Asp Ala Ser Thr Trp Ser Gln Ile
            260                 265                 270
Pro Pro Glu Asp Thr Ala Ser Thr Arg Ser Ser Phe Thr Val Gln Asp
    275                 280                 285
Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg Ile Arg Cys Met Lys Glu
    290                 295                 300
Asp Gly Lys Gly Tyr Trp Ser Asp Trp Ser Glu Glu Ala Ser Gly Ile
305                 310                 315                 320
Thr Tyr Glu Asp Arg Pro Ser Lys Ala Pro Ser Phe Trp Tyr Lys Ile
            325                 330                 335
Asp Pro Ser His Thr Gln Gly Tyr Arg Thr Val Gln Leu Val Trp Lys
            340                 345                 350
Thr Leu Pro Pro Phe Glu Ala Asn Gly Lys Ile Leu Asp Tyr Glu Val
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69

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          355                    360                    365
Thr Leu Thr Arg Trp Lys Ser His Leu Gln Asn Tyr Thr Val Asn Ala
    370                    375                    380
Thr Lys Leu Thr Val Asn Leu Thr Asn Asp Arg Tyr Leu Ala Thr Leu
385                    390                    395                    400
Thr Val Arg Asn Leu Val Gly Lys Ser Asp Ala Ala Val Leu Thr Ile
                405                    410                    415
Pro Ala Cys Asp Phe Gln Ala Thr His Pro Val Met Asp Leu Lys Ala
            420                    425                    430
Phe Pro Lys Asp Asn Met Leu Trp Val Glu Trp Thr Thr Pro Arg Glu
            435                    440                    445
Ser Val Lys Lys Tyr Ile Leu Glu Trp Cys Val Leu Ser Asp Lys Ala
    450                    455                    460
Pro Cys Ile Thr Asp Trp Gln Gln Glu Asp Gly Thr Val His Arg Thr
465                    470                    475                    480
Tyr Leu Arg Gly Asn Leu Ala Glu Ser Lys Cys Tyr Leu Ile Thr Val
                485                    490                    495
Thr Pro Val Tyr Ala Asp Gly Pro Gly Ser Pro Glu Ser Ile Lys Ala
            500                    505                    510
Tyr Leu Lys Gln Ala Pro Pro Ser Lys Gly Pro Thr Val Arg Thr Lys
            515                    520                    525
Lys Val Gly Lys Asn Glu Ala Val Leu Glu Trp Asp Gln Leu Pro Val
    530                    535                    540
Asp Val Gln Asn Gly Phe Ile Arg Asn Tyr Thr Ile Phe Tyr Arg Thr
545                    550                    555                    560
Ile Ile Gly Asn Glu Thr Ala Val Asn Val Asp Ser Ser His Thr Glu
                565                    570                    575
Tyr Thr Leu Ser Ser Leu Thr Ser Asp Thr Leu Tyr Met Val Arg Met
            580                    585                    590
Ala Ala Tyr Thr Asp Glu Gly Gly Lys Asp Gly Pro Glu Phe Thr Phe
            595                    600                    605
Thr Thr Pro Lys Phe Ala Gln Gly Glu Ile Glu Ala Ile Val Val Pro
    610                    615                    620
Val Cys Leu Ala Phe Leu Leu Thr Thr Leu Leu Gly Val Leu Phe Cys
625                    630                    635                    640
Phe Asn Lys Arg Asp Leu Ile Lys Lys His Ile Trp Pro Asn Val Pro
                645                    650                    655
Asp Pro Ser Lys Ser His Ile Ala Gln Trp Ser Pro His Thr Pro Pro
            660                    665                    670
Arg His Asn Phe Asn Ser Lys Asp Gln Met Tyr Ser Asp Gly Asn Phe
            675                    680                    685
Thr Asp Val Ser Val Val Glu Ile Glu Ala Asn Asp Lys Lys Pro Phe
    690                    695                    700
Pro Glu Asp Leu Lys Ser Leu Asp Leu Phe Lys Lys Glu Lys Ile Asn
705                    710                    715                    720
Thr Glu Gly His Ser Ser Gly Ile Gly Gly Ser Ser Cys Met Ser Ser
                725                    730                    735
Ser Arg Pro Ser Ile Ser Ser Ser Asp Glu Asn Glu Ser Ser Gln Asn
            740                    745                    750
Thr Ser Ser Thr Val Gln Tyr Ser Thr Val Val His Ser Gly Tyr Arg
            755                    760                    765
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70

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His Gln Val Pro Ser Val Gln Val Phe Ser Arg Ser Glu Ser Thr Gln
    770                 775                 780
Pro Leu Leu Asp Ser Glu Glu Arg Pro Glu Asp Leu Gln Leu Val Asp
785                 790                 795                 800
His Val Asp Gly Gly Asp Gly Ile Leu Pro Arg Gln Gln Tyr Phe Lys
                805                 810                 815
Gln Asn Cys Ser Gln His Glu Ser Ser Pro Asp Ile Ser His Phe Glu
            820                 825                 830
Arg Ser Lys Gln Val Ser Ser Val Asn Glu Glu Asp Phe Val Arg Leu
            835                 840                 845
Lys Gln Gln Ile Ser Asp His Ile Ser Gln Ser Cys Gly Ser Gly Gln
    850                 855                 860
Met Lys Met Phe Gln Glu Val Ser Ala Ala Asp Ala Phe Gly Pro Gly
865                 870                 875                 880
Thr Glu Gly Gln Val Glu Arg Phe Glu Thr Val Gly Met Glu Ala Ala
            885                 890                 895
Thr Asp Glu Gly Met Pro Lys Ser Tyr Leu Pro Gln Thr Val Arg Gln
            900                 905                 910
Gly Gly Tyr Met Pro Gln
            915
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